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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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1: /cgn2_6/ptodata/1,

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3: /cgn2_6/ptodata/1,

4: /cgn2_6/ptodata/1,

5: /cgn2_6/ptodata/1,

6: /cgn2_6/ptodata/1,
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/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/BCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
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US-08-284-586-2
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US-08-929-839-2
US-08-92-493-6
US-08-920-938-6
US-08-912-655-6
US-08-805-478-6
US-08-805-478-6
US-08-805-287-658-6
US-08-805-287-658-6
US-08-805-678-6
US-08-801-238-6
US-08-801-238-6
US-08-801-238-6
US-08-801-238-6
US-08-801-238-6
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US-08-801-238-6
US-08-982-493-8
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US-08-390-0008-5
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US-08-202-056-7
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ALIGNMENTS

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US-08-709-838-2
                                                                                                      Matches
                                                                                                                        Query Match
Best Local :
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                                                                                                                                                                                                                                                              TELEFAX: (617) 861-954
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE:
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: TK196-01
TELEPHONE: (617) 861-6240
                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION NAME: Brook Esq., David REGISTRATION NUMBER: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: MOSER, BERNHARD
TITLE OF INVENTION: IP-10/MIG RECEPTOR DESIGNATED CXCR3,
TITLE OF INVENTION: NUCLEIC ACIDS, AND METHODS OF USES THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Loetscher, Marcel APPLICANT: Moser, Bernhard
111 FLLGLLGNGAVAAVLLSRTALSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGL 170
                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: Two Mili
                                                                                                                      Local Similarity
                                                                                                                                                                                                                                             LENGTH:
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                                EVSDHQVLNDAEVAALLENFSSSYDYGENESDSCCTSPPCPQDFSLNFDRAFLPALYSLL 63
                                                                                                                                                                                                                           amino acid
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                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION:
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, 861-9540
, NO: 2:
                                                                                                                     87.9%;
99.7%;
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                                                                                                                                                                                                                                                                                                                                                                    22,592
                                                                                                    Score 1891; DB 4;
Pred. No. 2.3e-148;
1; Mismatches 0;
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                                                                     MOLECULE TYPE:
US-08-829-839-2
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US-08-829-839-2
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                                     Query Match
                                                                                                                                                                                                                                 FILING DATE: 31-MAR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/709,838
FILING DATE: 10-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Brook Esq., David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: TK196-01A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Loetscher, Marcel
APPLICANT: Moser, Bernhard
APPLICANT: Qin, Shixin
APPLICANT: Mackay, Charles R.
TITLE OF INVENTION: IP-10/MIG RECEPTOR DESIGNATED CXCR3,
TITLE OF INVENTION: ANTIBODIES, NUCLEIC ACIDS, AND METHODS OF USE THEREFOR
                                                                                   TYPE: amino acids
TOPOLOGY: line
WOLECHTP
                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS: ADDRESSEE: Hamilton,
                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Lexington STATE: MA
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     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, Version #1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/829,839
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     Conservative
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                 87.9%;
99.7%;
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                 Score 1891; DB 4; Length 368; Pred. No. 2.3e-148;
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                                  ; MOLECULE TYPE: US-08-982-493-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Gunn, Michael D
APPLICANT: Williams, Lewis T
APPLICANT: Cyster, Jason G
TITLE OF INVENTION: Modulatin
TITLE OF INVENTION: Receptor
                                                                                                                                 TELEFAX: (650) 343-43 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                       CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
NAME: OSMAN, RICHARD 36,627
                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                 SEQUENCE CHARACTERISTICS: LENGTH: 374 amino acids
                                                                                                                                                                               REFERENCE/DOCKET NUMBER: UC
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE:
                                                               TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: HILLSBOROUGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
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                                                                                amino acid
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                                                                                                                                                                (650) 343-4341
                                               protein
                                                                                                                                                  343-4342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Modulating B Lymphocyte Chemokine Receptor Interactions
 29.8%;
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 Score 640;
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Length 374;
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Matches

Gaps

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TOPOLOGY: US-08-202-056-5
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Patent No. 5440021
GENERAL INFORMATION:
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                                                                                                                                                                                                        APPLICATION NUMBER: US/08/202,056
EILING DATE: 25-FEB-1994
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/677211
EILING DATE: 29-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: LOVE, RICHART B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: 706P3
                                                                                 TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Lee, James
TITLE OF INVENTION: Antibodies to Human IL-8 Type B Receptor
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Chuntharapal, Anan APPLICANT: Hebert, Caroline
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        190 ACISEDRYLNIVHATQLYRRGPPARVTLTCLAVWGLCLLFALPDEIFLSA---HHDERLN 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      130 TALSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGLCKVAGALFNINFYAGALLL 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         247 ATHCOYNFPOVGRT----ALRVLOLVAGFILPLLVMAYCYAHILAVLL-VSRGQRRLRAM 301
                                        TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26 YSNSTEIPLQDSNFCST---VEGPLLTSFKAVFMPVAYSLIFLLGMMGNILVLVILERHR 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PMLYTFAGVKFRSDLSRLLTKLGCAGPASL-CQLFPNWRKSSLSESENAT 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSSWSETSEAS 411
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RLVVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVTSGLGYMHCCLN 361
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                                                                372 amino acids
                                                                                                                                                  2: 415/225-5530
415/952-9881
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genentech,
                                                                                                                                                                                                                                                                                                                                                                                                                                                            PC-DOS/MS-DOS
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54; Mismatches 139;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local
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                     INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
APPLICANT:
                                                                                                                                     FILING DATE: 29-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B
REGISTRATION NUMBER: 34,659
                                                                                                                                                                                                                     APPLICATION NUMBER: 07/8 FILING DATE: 19-DEC-1991 PRIOR APPLICATION DATA: APPLICATION NUMBER: 07/6
                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genentech) CURRENT APPLICATION DATA:
SEQUENCE CHARACTERISTICS:
                                                                                                 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Antibodies to Human PF4A Receptors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 415/-7168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  292 SRGQRRLRAMRLVVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVTS 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             131 VNFYCSSLLLACIAVDRYLAIVHAVHAYRHRRLLSIHITCGTIWLVGFLLALPEILFAKV 190
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                                                                                                                                                                                                                                                                                                                                 FILING DATE: 11 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: South San Francisco
STATE: California
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                                                            TELEPHONE: 415/225-5530
TELEFAX: 415/952-9881
                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/076,093A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               71
                                                                                                                          REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11 LENLEDLFWELDRLDNYNDTSLVENHLCPATEGPLMASFKAVFVPVAYSLIFLLGVIGNV 70
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Pred. No. 6.5e-45;
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RESULT 6
US-08-701-265-6
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; TOPOLOGY:
US-08-076-093A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 6, Application US/08701265 Patent No. 5776457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 29.5%;
Best Local Similarity 40.8%;
Matches 147; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                   APPLICATION NUMBER: 07/67721
FILING DATE: 29-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: LOVE, Richard B
REGISTRATION NUMBER: 34,659
                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
                                                                                                                                                                                               APPLICATION NUMBER: US/08/701.
FILING DATE: 22-AUG-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/076093
FILING DATE: 11-Jun-1993
                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genentech) CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: NUMBER OF SEQUENCES:
      TELECOMMUNICATION
                                                                                                                                        PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                309
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                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 460 Point San Bruno
CITY: South San Francisco
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                    REFERENCE/DOCKET NUMBER:
                                                                                                                                                              FILING DATE:
                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
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Hebert, Caroline
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                                                                                                                                                              19-DEC-1991
    INFORMATION:
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                                                                                                                                                                                 07/810782
                                                                                                                       07/677211
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Pred. No. 6.5e-45;
                      706P2
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Best Local Similarity
Matches 147; Conserv
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TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
LENGTH: 372 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Chuntharapai, Anan
APPLICANT: Lee, James
APPLICANT: Hebert, Caroline
APPLICANT: Jin Kim, K.
TITLE OF INVENTION: Antibodies
                                                                                                                                                                ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/284,586
                CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/076,093A
FILING DATE: 11-Jun-1993
APPLICATION NUMBER: 07/810782
FILING DATE: 19-DEC-1991
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         352 GLGYMHCCLNPLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSSWSETSEAS 411
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                                                                                                                                                          FILING DATE:
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CITY: South San Francisco
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67 LENFSSSY---DYGENESD-SCCTSPPCPQ---DFSLNFDRAFLPALYSLLFLLGLLGNG 119
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40.8%; Pred. No. 6.5e-45;
vative 50; Mismatches 145;
07/677211
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Bruno
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FILING DATE: 29-MAR-1991 ATTORNEY/AGENT INFORMATION:

NAME: Love, Richard B REGISTRATION NUMBER:

REFERENCE/DOCKET NUMBER:

34,659

706P2

8

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Sequence 6, Application US/08805478

Patent NO. 5874543

GENERAL INFORMATION:

APPLICANT: Chuntharapai, Anan
APPLICANT: Hebert, Caroline
APPLICANT: Jin Kim, K.

TITLE OF INVENTION: ANTIBODIES TO PF4A RECEPTOR
NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
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                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: WinPatin (Genentech)
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LENGTH: 372 amino acids
TYPE: Amino Acid
                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/805,478
FILING DATE: 25-Feb-1997
CLASSIFICATION: 530
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TELEPHONE: 415/225-5530
TELEFAX: 415/952-9881
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les 147; Conserv
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TELEX: 910/371-7168
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APPLICATION DATA:
                                                                                                                                                                                                   94080
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RESULT 9
US-08-802-627A-6
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                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
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                                                                                                                                                                    APPLICANT: Lee, James
APPLICANT: Wood, William I.
APPLICANT: Wood, WILLIAM I.
TITLE OF INVENTION: NUCLEIC ACID ENCODING PF4A RECEPTOR NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ANDRESSEE: Genentech, Inc.
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: PO TELECOMMUNICATION INFORMATION: TELEPHONE: 415/225-5530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 19-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              249 QRRPQRQKAVRVAILVTSIFFLCWSPYHIVIFLDTLARLKAVDNTCKLNGSLPVAITMCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          191 SQGHHNNSL--PRCTFSQENQAETHAWFTSRFLYHVAGFLLPMLVMGWCYVGVVHRLRQA 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      131 VNFYCSSLLLACIAVDRYLAIVHAVHAYRHRRLLSIHITCGTIWLVGFLLALPEILFAKV 190
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                                                                                                                                             STREET: 460 Point San Bruno
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                71 LVLVILERHRQTRSSTETFLFHLAVADLLLVFILPFAVAEGSVGWVLGTFLCKTVIALHK 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 372 amino acids TYPE: Amino Acid
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                                                                                                                               COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 08/0
FILING DATE: 11-JUN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: FILING DATE: 10-AUC
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RESULT 10
US-08-801-238-6
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Patent No. 5919896
GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
                                                                                                         TITLE OF INVENTION: PF4A RECEPTOR NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
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LENGTH: 372 amino acid
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TELEPHONE: 415/225-5530
TELEFAX: 415/952-9881
                                                                                                                                                              APPLICANT: Lee, James
APPLICANT: Wood, William I.
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                             STREET: 460 Point San Bruno Blvd CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                      309 FLGLAHCCLNPMLYTFAGVKFRSDLSRLLTKLGCTGPASLCQLFPSWRR-SSLSESENAT 367
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COUNTRY: UZIP: 94080
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les 147; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -SAHHDERLNATHCQYNFPQVGRT----ALRVLQLVAGFLLPLLVMAYCYAHILAVL-LV 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VNFYCSSLLLACIAVDRYLAIVHAVHAYRHRRLLSIHITCGTIWLVGFLLALPEILFAKV 190
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                   USA
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19-DEC-1991
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RESULT 11
US-08-801-228-6
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                                                                                                              Sequence 6, Application US/08801228 Patent No. 5922541
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
GENERAL INFORMATION:
APPLICANT: Lee, James
APPLICANT: Wood, William I.
TITLE OF INVENTION: METHODS FOR DETECTION AND AMPLIFICATION
TITLE OF INVENTION: PF4A RECEPTOR NUCLEIC ACID
NUMBER OF SEQUENCES: 6
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NAME: Love, Richard B.
REGISTRATION NUMBER: 34,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/81
FILING DATE: 19-DPC-10-1
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APPLICATION NUMBER: US/0
FILING DATE: 19-Feb-1997
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MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: POTELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 530
PRIOR APPLICATION DATA:
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APPLICATION NUMBER:
                                                                                                                                                                                                                            249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: Amino Acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11 LENLEDLFWELDRLDNYNDTSLVENHLCPATEGPLMASFKAVFVPVAYSLIFLLGVIGNV 70
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TELEFAX: 415/952-9881
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             VNFYCSSLLLACIAVDRYLAIVHAVHAYRHRRLLSIHITCGTIWLVGFLLALPEILFAKV 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFYAGALLLACISFDRYLNIVHATQLYRRGPPARVTLTCLAVWGLCLLFALPDFIFL--
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                                                                                                                                                                                                                                                                                                                                        SRGQRRLRAMRLVVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVTS
                                                                                                                                                                                                                                                                                                                                                                                  SQGHHNNSL--PRCTFSQENQAETHAWFTSRFLYHVAGFLLPMLVMGWCYVGVVHRLRQA
                                                                                                                                                                                                                                                                                                                                                                                                                     -SAHHDERLNATHCQYNFPQVGRT----ALRVLQLVAGFLLPLLVMAYCYAHILAVL-LV 291
                                                                                                                                                                                                                                                                                                       QRRPQRQKAVRVAILVTSIFFLCWSPYHIVIFLDTLARLKAVDNTCKLNGSLPVAITMCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       372 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Linear
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Pred. No. 6.5e-45;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         145;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18;
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CORRESPONDENCE ADDRESS

ADDRESSEE:

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RESULT 12
US-09-104-296-6
; Sequence 6, Application US/09104296
; Patent No. 6087475
; GENERAL INFORMATION:
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REFERENCE/OCKET NUMBER: P070
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5530
TELEFAX: 415/952-9881
TELEFX: 910/371-7168
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/284'
APPLICATION NUMBER: 10-AUG-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 19-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 11-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/8
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                                                                                                                                                               352 GLGYMHCCLNPLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSSWSETSEAS 411
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67 LENFSSSY----DYGENESD-SCCTSPPCPQ---DFSLNFDRAFLPALYSLLFLLGLLGNG 119
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Local Similarity 40.8%;
es 147; Conservati
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH:
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                                                                                                                                                                                                   AVAAVLLSRRTALSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGLCKVAGALFN 179
                                                                                                                              FLGLAHCCLNPMLYTFAGVKFRSDLSRLLTKLGCTGPASLCQLFPSWRR-SSLSESENAT 367
                                                                                                                                                                                                                                        SRGQRRLRAMRLVVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVTS 351
                                                                                                                                                                                                                                                                            SQGHHNNSL--PRCTFSQENQAETHAWFTSRFLYHVAGFLLPMLVMGWCYVGVVHRLRQA 248
                                                                                                                                                                                                                                                                                             -SAHHDERLNATHCQYNFPQVGRT----ALRVLQLVAGFLLPLLVMAYCYAHILAVL-LV 291
                                                                                                                                                                                                                                                                                                                                                                                       INFYAGALLLACISFDRYLNIVHATQLYRRGPPARVTLTCLAVWGLCLLFALPDFIFL-- 237
                                                                                                                                                                                                                                                                                                                                                                                                                        LVLVILERHRQTRSSTETFLFHLAVADLLLVFILPFAVAEGSVGWVLGTFLCKTVIALHK 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENLEDLFWELDRLDNYNDTSLVENHLCPATEGPLMASFKAVFVPVAYSLIFLLGVIGNV 70
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Amino Acid
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19-DEC-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50; Mismatches 145; Indels 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 635; DB 2;
Pred. No. 6.5e-45;
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Matches 147; Conservation
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TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 372 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: PO
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 11-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/8
FILING DATE: 19-DEC-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: 3.5 inch, 1.44 mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genentech) CURRENT APPLICATION DATA:
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APPLICATION NUMBER:
FILING DATE: 06-JUN-
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COMPUTER READABLE FORM:
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CORRESPONDENCE ADDRESS:
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APPLICATION NUMBER:
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                                                                                                                                                                                                                  131 VNFYCSSLLLACIAVDRYLAIVHAVHAYRHRRLLSIHITCGTIWLVGFLLALPEILFAKV 190
352 GLGYMHCCLNPLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSSSWSETSEAS
                                                            249 QRRPQRQKAVRVAILVTSIFFLCWSPYHIVIFLDTLARLKAVDNTCKLNGSLPVAITMCE 308
                                                                                                                                                                                                                                                                                                                    120 AVAAVLLSRRTALSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGLCKVAGALFN 179
                                                                                                                                                                                                                                                                                                 71
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                                                                                                                                                                                                                                                                                                                                                                            11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 34,659
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                                                                                                                                       SQGHHNNSL--PRCTFSQENQAETHAWFTSRFLYHVAGFLLPMLVMGWCYVGVVHRLRQA 248
                                                                                                                                                            -SAHHDERLNATHCQYNFPQVGRT----ALRVLQLVAGFLLPLLVMAYCYAHILAVL-LV 291
                                                                                                                                                                                                                                                       INFYAGALLLACISFDRYLNIVHATQLYRRGPPARVTLTCLAVWGLCLLFALPDFIFL-- 237
                                                                                               SRGQRRLRAMRLVVVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVTS 351
                                                                                                                                                                                                                                                                                             LVLVILERHRQTRSSTETFLFHLAVADLLLVFILPFAVAEGSVGWVLGTFLCKTVIALHK 130
                                                                                                                                                                                                                                                                                                                                                                          LENLEDLFWELDRLDNYNDTSLVENHLCPATEGPLMASFKAVFVPVAYSLIFLLGVIGNV 70
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Wood, WIlliam
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Richard B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-JUN-1996
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US-08-982-493-8
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APPLICANT: Gunn,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (650) 343-43 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
ATTORNBY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: UC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Rel CURRENT APPLICATION DATA:
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ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 75 DENISE DRIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Williams, Lewis APPLICANT: Cyster, Jason G TITLE OF INVENTION: Modulat TITLE OF INVENTION: Receptch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
    309
                                   352 GLGYMHCCLNPLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSSWSETSEAS 411
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                                                                                                                                                                                                                                           131
                                                                                                                                                                                                                                                                            180 INFYAGALLLACISFDRYLNIVHATQLYRRGPPARVTLTCLAVWGLCLLFALPDFIFL-- 237
                                                                                                                                                                                                                                                                                                                                            120 AVAAVLLSRRTALSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGLCKVAGALFN 179
                                                                                                                 292 SRGQRRLRAMRLVVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVTS 351
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                       67 LENFSSSY---DYGENESD-SCCTSPPCPQ---DFSLNFDRAFLPALYSLLFLLGLLGNG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity es 147; Conserv
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FLGLAHCCLNPMLYTFAGVKFRSDLSRLLTKLGCTGPASLCQLFPSWRR-SSLSESENAT
                                                                                                                                                                                                                                                                                                                    LVLVILERHRQTRSSTETFLFHLAVADLLLVFILPFAVAEGSVGWVLGTFLCKTVIALHK 130
                                                                                                                                                                                                                                                                                                                                                                                                  LENLEDLFWELDRLDNYNDTSLVENHLCPATEGPLMASFKAVFVPVAYSLIFLLGVIGNV 70
                                                                                                                                                                                                                                       VNFYCSSLLLACIAVDRYLAIVHAVHAYRHRRLLSIHITCGTIWLVGFLLALPEILFAKV 190
                                                                            QRRPQRQKAVRVAILVTSIFFLCWSPYHIVIFLDTLARLKAVDNTCKLNGSLPVAITMCE 308
                                                                                                                                                           SQGHHNNSL--PRCTFSQENQAETHAWFTSRFLYHVAGFLLPMLVMGWCYVGVVHRLRQA 248
                                                                                                                                                                                                -SAHHDERLNATHCQYNFPQVGRT----ALRVLQLVAGFLLPLLVMAYCYAHILAVL-LV 291
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ilarity 40.8%;
Conservative !
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   343-4342
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Score 635; DB 3; I; Pred. No. 6.5e-45; 50; Mismatches 145;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 372;
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US-07-759-568-1
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Best Local Similarity
Matches 141; Conserv
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Patent No. 5374506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: 6714627 cush INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: RSCOLT, Watson T.
REGISTRATION NUMBER: 26581
REFERENCE/DOCKET NUMBER: WTS,
TELECOMMUNICATION INFORMATION:
TELEPHNE: 202-861-3000
TELEFAX: 202-822-0944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
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TITLE OF INVENTION: Cloning of cDNA Encoding a Functional
TITLE OF INVENTION: Human Interleukin-8 Receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
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  301
                                                                             241
                                                                                                                                                           185 SNVSPA-C---YEDMGNNTANWRMLLRILPQSFGFIVPLLIMLFCYGFTLRTLFKAHMGQ
                                                                                                                                                                             135
                                                                                                                                                                                                                                                           192 ISFDRYLNIVHATQLYRRGPPARVTLT-------CLAVWGLCLLFALPDFIFLSAHHD 242
                                                                                                                                                                                                                                                                                                                                       132 LSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGLCKVAGALENINFYAGALLLAC 191
                                    357 HCCLNPLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSSWSETS 408
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TOPOLOGY: li
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                                                                                                                                                                                                                                                                                                                                                                                                                                     72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                    SSYDYGENESDSCCTSPPCPQDFSLNFDRAFLPALYSLLFLLGLLGNGAVAAVLLSRRTA 133
                                                                           KHRAMRVIFAVVLIFLLCWLPYNLVLLADTLMRTQVIQETCERRNHIDRALDATEILGIL
HSCLNPLIYAFIGQKFRHGLLKILAIHGLISKDSLPKDSRPSFVGSSSGHTS
                                                                                                                  RLRAMRLVVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVTSGLGYM 356
                                                                                                                                                                                                                                                                                                                  RSVTDVYLLNLALADLLFALTLPIWAASKVNGWIFGTFLCKVVSLLKEVNFYSGILLLAC 134
                                                                                                                                                                                                                                     ISVDRYLAIVHATR-----TLTQKRYLVKFICLSIWGLSLLLALPVLLFRRTVYS 184
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1615 L Street, N.W.
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Pred. No. 9e-45;
1; Mismatches 1
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Search completed: November Job time : 28 secs
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Best Local Similarity 40.1
Matches 141; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/450,393A
FILING DATE: May 25, 1995
CLASSIFICATION: 424
ATTORNEY, AGENT INFORMATION:
NAME: CSerr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: UCAL-237/02US
TELECOMMUNICATION INFORMATION:
TELEFAX: 415-843-5165
TELEFAX: 415-8657-0663
TELEFAX: 415-8657-0663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy d.sk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 355 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
STREET: 5 Palo Alto Square
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Charo, Israel
APPLICANT: Coughlin, Shaun
TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
TITLE OF INVENTION: PROTEIN RECEPTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE:
HYPOTHETICAL:
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                                                                                                                                                 243 ERLNATHCQYNFPQVG-----RTALRVLQLVAGFLLPLLVMAYCYAHILAVLLVSRGQR 296
                                                                         301 HSCLNPLIYAFTGQKFRHGLLKILAIHGLISKDSLPKDSRPSFVGSSSGHTS 352
                                                                                                                                                                                                                                 185 SNVSPA-C---YEDMGNNTANWRMLLRILPQSFGFIVPLLIMLFCYGFTLRTLFKAHMGQ 240
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STATE: California
                                                                                                                                                                                                                                                                                                                                                                                           75 RSVTDVYLLNLALADLLFALTLPIWAASKVNGWIFGTFLCKVVSLLKEVNFYSGILLLAC 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
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                                                                                                              HCCLNPLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSSWSETS 408
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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-OB-ISSued_Patents_Na -OPMT-fastap -SUFFIX-ppn rni -MINMATCH-0.1 -LOOPCL-0
-LOOPCXT-0 -UNITS-blts -START-1 -END-1 -MATRIX-blosum62 -TRANS-human40 .cdi
-LIST-45 -DOCALIGN-200 -THR_SCORE-pct -THR_MAX-100 -THR_MIN-0 -ALIGN-15
-MODE-LOCAL -OUTFMT-pto -NORM-ext -HEAPSIZE-500 -MINLEN-0 -MAXLEN-20000000
-USER-US09101518_@CGN_11_13_@runat_29102002_091056_29932 -NCPU-6 -ICPU-3
-NORE-US09101518_@CGN_11_13_@runat_29102002_091056_29932 -NCPU-6 -ICPU-3
-NARN_TIMEOUT-30 -THREADS-1 -XGAPOP-10 -WART-O.5 -FGAPOP-6 -FGAPEXT-7
-NARN_TIMEOUT-30 -THREADS-1 -XGAPOP-10 -WART-O.5 -FGAPOP-6 -FGAPEXT-7
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1: /cgn2_6/ptodata/
2: /cgn2_6/ptodata/
3: /cgn2_6/ptodata/
4: /cgn2_6/ptodata/
5: /cgn2_6/ptodata/
6: /cgn2_6/ptodata/
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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2151
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   GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                    /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/BCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/backfiles1.seq:*
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   1670
1670
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            US-08-709-838-1
US-08-929-839-1
US-08-92-493-5
US-07-759-568-4
US-08-202-056-6
US-08-201-265-5
US-08-01-265-5
US-08-801-238-5
US-08-801-238-5
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2080.365 Million cell updates/sec
Sequence
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Appli
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ALIGNMENTS

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Sequence 1, Application US/08709838 Patent No. 6140064 GENERAL INFORMATION:
                                                                           ATTORNEY AGENT INFORMATION:
NAME: Brook Esq., David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: TKI9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
                                     TELEFAX: (617) 861-954
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                          ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: LOETSCHEI, APPLICANT: LOETSCHEI, APPLICANT: MOSER, Bernhard
TITLE OF INVENTION: IP-10/MIG RECEPTOR DESIGNATED CXCR3,
TITLE OF INVENTION: NUCLEIC ACIDS, AND METHODS OF USES THEREFOR
                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
SEQUENCE CHARACTERISTICS LENGTH: 1670 base pai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                APPLICATION NUMBER: FILING DATE:
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ZIP: 02173
                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: Two Mil CITY: Lexington STATE: MA
                                                                                                                                                                                                                CLASSIFICATION: 530
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                                                              (617) 861-9540
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FEATURE:
NAME/KEY:
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STRANDEDNESS: double
TOPOLOGY: unknown
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LeuSerAlaHisHisAspGluArgLeuAsnAlaThrHisCysGlnTyrAsnPheProGln
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                                                                                                                                                                                                                                                                            ValMetAlaTyrCysTyrAlaHisIleLeuAlaValLeuLeuValSerArgGlyGlnArg
                                                                    AsnPheAspArgAlaPheLeuProAlaLeuTyrSerLeuLeuPheLeuLeuGlyLeuLeu 116
                              GTCATGGCCTACTGCTATGCCCACATCCTGGCCGTGCTGCTGGTTTCCAGGGGCCAGCGG
                                                            CTGTCGGCCCACCACGAGGGCGCCTCAACGCCACCCACTGCCAATACAACTTCCCACAG
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97.63%
97.36%
88.19%
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                                                                US-08-829-839-1
                                                                                                                                                                                     APPLICATION NUMBER: US 08/709
FILING DATE: 10-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Brook Esq., David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: TKI9
TELECOMMUNICATION INFORMATION:
TELEPAN: (617) 861-6240
TELEPAN: (617) 861-9540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
IFMORTH 1670 hade nairs
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APPLICANT: Loetscher, Marcel
APPLICANT: Moser, Bernhard
APPLICANT: Moser, Bernhard
APPLICANT: Qin, Shixin
APPLICANT: Mackay, Charles R.
TITLE OF INVENTION: IN-10/MIG RECEPTOR DESIGNATED CXCR3,
TITLE OF INVENTION: ANTIBODIES, NUCLEIC ACIDS, AND METHODS OF USE THEREFOR NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, V.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/829,839
FILING DATE: 31-MAR-1997
                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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ADDRESSEE: Hamilton, Brook,
STREET: Two Militia Drive
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                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: double
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HisCysCysLeuAsnProLeuLeuTyrAlaPheValGlyValLysPheArgGluArgMet
                                   CysGlyArgGluSerArgValAspValAlaLysSerValThrSerGlyLeuGlyTyrmet
                                                                   ProTyrHisLeuValValLeuValAspIleLeuMetAspLeuGlyAlaLeuAlaArgAsn
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                          TGTGGCCGAGAAAGCAGGGTAGACGTGGCCAAGTCGGTCACCTCAGGCCTGGGCTACATG
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FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: UCSF
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 343-4341
TELEPAX: (650) 343-4342
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
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APPLICANT: Gunn, Michael D

APPLICANT: Gunl, Michael D

APPLICANT: Cyster, Jason G

TITLE OF INVENTION: Modulati

TITLE OF INVENTION: Receptor
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS: SCIENCE & TECHNOLOGY
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CITY: HILLSBOROUGH
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94010
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                           CysProGlnAspPheSerLeuAsnPheAspArgAlaPheLeuProAlaLeuTyrSerLeu
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RESULT 4
US-07-759-568-4
(Sequence 4, Application US/07759568
; Patent No. 5374506
; GENERAL INFORMATION:
; APPLICANT: Murphy, Philip M.
; TITLE OF INVENTION: Cloning of cDNA Encoding a Functional
; TITLE OF INVENTION: Human Interleukin-8 Receptor
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                                                                                                                                            AGTAGTCTCTGAGTCAGAGAATGCTACT 1107
                                                                                                                                                                          SerSerTrpSerGluThrSerGluAlaSer 411
                                                                                                                                                                                                      AAGCTGGGCTGTGCTGGCCCGGCCTCCCTT---TGCCAACTTTTCCCCAACTGGCGCAAG 1077
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Best Local Similarity:
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TELEX: 6714627 cush
INFORMATION FOR SEQ ID NO:
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FILING DATE: 19910913
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: SCOTT, WATSON T.
REGISTRATION NUMBER: 26581
REFERENCE/DOCKET NUMBER: W
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MOLECULE TYPE:
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LENGTH: 1510 base pairs
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CORRESPONDENCE ADDRESS:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                   ValPheGlySerGlyLeuCysLysValAlaGlyAlaLeuPheAsnIleAsnPheTyrAla ::::||||||::: |||||||||:::
GlyAlaLeuLeuAlaCysIleSerPheAspArgTyrLeuAsnIleValHisAlaThr
                                LeuLeuSerArgArgThrAlaLeuSerSerThrAspThrPheLeuLeuHisLeuAlaVal 144
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                                                                                                                                 AlaAspThrLeuLeuValLeuThrLeuProLeuTrpAlaValAspAlaAlaValGlnTrp
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Matches:
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US-08-202-056-6
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                                      COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                APPLICANT: Kim, Kyung Jin
APPLICANT: Lee, James
TITLE OF INVENTION: Antibodies
NUMBER OF SEQUENCES: 8
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CITY: South San Francisco
STATE: California
COUNTRY: USA
       FILING DATE:
                            APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LeuGlyAlaLeuAlaArgAsnCysGlyArgGluSerArgValAspValAlaLysSerVal 349
                                                                                                                                                                                           94080
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460 Point San Bruno Blvd
       25-FEB-1994
                        US/08/202,056
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Best Local Similarity:
Query Match:
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TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 1679 bases
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ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 70
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: 415/225-5530
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CAAGCAGAAACGCATGCCTGGTTCACCTCCCGATTCCTCTACCATGTGGCGGGATTCCTG
                                                                                                                                                                                                         LeuAlaValTrpGlyLeuCysLeuLeuPheAlaLeuProAspPheIlePheLeu-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGCTCTGTGGGCTGGGTCCTGGGGACCTTCCTCTGCAAAACTGTGATTGCCCTGCACAAA 758
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                                           ValGlyArgThr------AlaLeuArgValLeuGlnLeuValAlaGlyPheLeu
                                                                                           AGCCAAGGCCATCACAACAACTCCCTG-----CCACGTTGCACCTTCTCCCAAGAGAAC
                                                                                                                                                                                      GGGACCATCTGGCTGGGCTTCCTCCTTGCCTTGCCAGAGATTCTCTTCGCCAAAGTC
                                                                                                                                                                                                                                                                                                                        IleValHisAlaThrGlnLeuTyrArgArgGlyProProAlaArgValThrLeuThrCys 219
                                                                                                                                                                                                                                                                                                                                                                                                IleAsnPheTyrAlaGlyAlaLeuLeuAlaCysIleSerPheAspArgTyrLeuAsn 199
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Matches:
Conservative:
Mismatches:
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RESULT 6
US-08-076-093A-5
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                                    TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
COMPUTER: SYSTEM: PC-DOS/MS-DOS
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APPLICANT:
APPLICANT:
APPLICANT:
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SEQUENCE CHARACTERISTICS: LENGTH: 1679 nucleotic
                                                                                          REFERENCE/DOCKET NUMBER: 70
TELECOMMUNICATION INFORMATION: 415/225-5530
                                                                                                                                                                                        APPLICATION NUMBER: 07/67
FILING DATE: 29-MAR-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                   FILING DATE: 19-DEC-PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
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                                                               TELEPHONE: 415/223-33.
TELEFAX: 415/952-9881
                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/076,093A FILING DATE: 11-Jun-1993 CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
                                                                                                                                                     NAME: Love, Richard B
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 07/8 FILING DATE: 19-DEC-1991
                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM:
SOFTWARE: WinPati
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Best Local Similarity:
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STRANDEDNESS: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LeuGluAsnPheSerSerTyr------AspTyrGlyGluAsnGluSerAsp---
                                                     TTCCTCTGCTGGTCACCCTACCACATCGTCATCTTCCTGGACACCCTGGCGAGGCTGAAG 1232
                                                                                                                                                                                                              CTGCCCATGCTGATGGGCTGGTGCTACGTGGGGGTAGTGCACAGGTTGCGCCAGGCC 1112
                                                                                                                                                                                                                                     LeuProLeuLeuValMetAlaTyrCysTyrAlaHisIleLeuAlaValLeu---LeuVal 291
              AlaLeuAlaArgAsnCysGlyArgGluSerArgValAspValAlaLysSerValThrSer 351
                                                                           AlaLeuCysTrpThrProTyrHisLeuValValLeuValAspIleLeuMetAspLeuGly 331
                                                                                                                                CAGCGGCGCCCTCAGCGGCAGAAGGCAGTCAGGGTGGCCATCCTGGTGACAAGCATCTTC 1172
                                                                                                                                                                                                                                                                                            CAAGCAGAAACGCATGCCTGGTTCACCTCCCGATTCCTCTACCATGTGGCGGGATTCCTG 1052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LeuAlaYalTrpGlyLeuCysLeuLeuPheAlaLeuProAspPheIlePheLeu-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTCCACCTGGCCGTGGCCGACCTCCTGCTGGTCTTCATCTTGCCCTTTGCCGTGGCCGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SerCysCysThrSerProProCysProGln-----AspPheSerLeuAsnPheAsp 99
                                                                                                                                                                     SerArgGlyGlnArgArgLeuArgAlaMetArgLeuValValValValValValAlaPhe 311
                                                                                                                                                                                                                                                                                                                      ValGlyArgThr-----AlaLeuArgValLeuGlnLeuValAlaGlyPheLeu 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGGACCATCTGGCTGGGCTTCCTCCTTGCCTTGCCAGAGATTCTCTTCGCCAAAGTC 938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IleValHisAlaThrGlnLeuTyrArgArgGlyProProAlaArgValThrLeuThrCys 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGCTCTGTGGGCTGGGTCCTGGGGGACCTTCCTCTGCAAAACTGTGATTGCCCTGCACAAA 758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCCCTGGTGGAAAATCATCTCTGCCCTGCCACAGAGGGGCCCCTCATGGCCTCCTTCAAG 518
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Sequence 5, Application US/08701265
Patent No. 5776457
GENERAL INFORMATION:
APPLICANT: Chuntharapai, Anan
APPLICANT: Lee, James
APPLICANT: Hebert, Caroline
APPLICANT: Min Kim, K.
                      Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                ; LENGTH: 1679 nucleo
TYPE: Nucleic Acid
; STRANDEDNESS: Sing
TOPOLOGY: Linear
US-08-701-265-5
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                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 706F
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/252-5530
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1679 nucleotides
TYDE: Nucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 19-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/6:
FILING DATE: 29-MAR-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/076093
FILING DATE: 11-Jun-1993
APPLICATION NUMBER: 07/810782
FILING DATE: 19-DEC-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Antibodies
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
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CITY: SO
STATE: C
COUNTRY:
ZIP: 940
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                                                                                                                                                                                                                                                                                                                                                                                    NAME: Love, Richard B
REGISTRATION NUMBER: 34,659
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T: 460 Point San Bruno
South San Francisco
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22-AUG-1996
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TGCCAGCTCTTCCCTAGCTGGCGCAGG---AGCAGTCTCTCTGAGTCAGAGAATGCCACC
                                                                                                                                                                GlyLeuGlyTyrMetHisCysCysLeuAsnProLeuLeuTyrAlaPheValGlyValLys 371
                                                                                                                                                                                                                                                                                                              AlaLeuCysTrpThrProTyrHisLeuValValLeuValAspIleLeuMetAspLeuGly 331
                                                                                                                                                                                                                                                                                                                                                                 CAGCGGCGCCCTCAGCGGCAGAAGGCAGTCAGGGTGGCCATCCTGGTGACAAGCATCTTC 1172
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                    PheArgGluArgMetTrpMetLeuLeuArgLeuGlyCysProAsnGlnArgGlyLeu 391
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              LeuProLeuLeuValMetAlaTyrCysTyrAlaHisIleLeuAlaValLeu---LeuVal 291
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                                                                     TTCCTGGGCCTGGCCACTGCTGCCTCAACCCCATGCTCTACACTTTCGCCGGCGTGAAG
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TOPOLOGY:
US-08-284-586-5
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TELEPHONE: 415/225-530
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1679 nucleotides
TYPE: Nucleic Acid
TYPE: Nucleic Acid
STRANDEDNESS: Single
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APPLICANT: Jin Kim, K.
TITLE OF INVENTION: Antibodies to Human PF4A Receptors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 07/6;
FILING DATE: 29-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B
REGISTRATION NUMBER: 34,6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 07/8 FILING DATE: 19-DEC-1991 PRIOR APPLICATION DATA:
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MEDIUM TYPE: 3.5 inch, 1.44 mb floppy
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
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FILING DATE: 10-Jun-1993
FILING DATE: 10-Jun-1993
FILING DATE: 10-Jun-1993
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REFERENCE/DOCKET NUMBER: 70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
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                              ArgAlaPheLeuProAlaLeuTyrSerLeuLeuPheLeuLeuGlyLeuLeuGlyAsnGly 119
                                                                                                                                                                           LeuGluAsnPheSerSerSerTyr------AspTyrGlyGluAsnGluSerAsp---
GCCGTGTTCGTGCCCGTGGCCTACAGCCTCATCTTCCTCCTGGGCGTGATCGGCAACGTC
                                                                                                                                            CTCGAGAACCTGGAGGACCTGTTCTGGGAACTGGACAGATTGGACAACTATAACGACACC
                                                                                                    SerCysCysThrSerProProCysProGln-----AspPheSerLeuAsnPheAsp 99
                                                                    TCCCTGGTGGAAAATCATCTCTGCCCTGCCACAGAGGGGCCCCTCATGGCCTCCTTCAAG
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Matches:
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Indels:
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                                                       GENERAL INFORMATION:
APPLICANT: Chuntharapai
APPLICANT: Lee, James
APPLICANT: Hebert, Carr
APPLICANT: Jin Kim, K.
                                                                                                                                                             Sequence 5, Application US/08805478 Patent No. 5874543
            APPLICANT: Jin Kim, K.
TITLE OF INVENTION: ANTIBODIES TO PF4A RECEPTOR
NUMBER OF SEQUENCES: 6
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CORRESPONDENCE ADDRESS
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                                                                          Hebert, Caroline
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TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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TELEPHONE: 415/225-5530
TELEFAX: 415/952-9881
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APPLICATION NUMBER: 07/81
FILING DATE: 19-DEC-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 08/21
FILING DATE: 10-AUG-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 530 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: 3.5 inc
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                                                                                                                                                     120 AlaValAlaAlaValLeuLeuSerArgArgThrAlaLeuSerSerThrAspThrPheLeu 139
                                                                                                                                                                                                            519
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699 GGCTCTGTGGGCTGGGTCCTGGGGACCTTCCTCTGCAAAACTGTGATTGCCCTGCACAAA 758
                            160 AlaAlaValGlnTrpValPheGlySerGlyLeuCysLysValAlaGlyAlaLeuPheAsn 179
                                                                                                                                                                                                                                                                                                             83
                                                                                                                                                                                                                                                                                                                                                                        67 LeuGluAsnPheSerSerTyr-----AspTyrGlyGluAsnGluSerAsp---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: Nucleic
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: PO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 08/0 FILING DATE: 11-JUN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: FILING DATE: 25-Fe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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CITY: South San Francisco
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                                                                                                                                   CTGGTGCTGGTGATCCTGGAGCGGCACCGGCAGACACGCAGTTCCACGGAGACCTTCCTG
                                                                                                                                                                                                                                                                                                                                           CTCGAGAACCTGGAGGACCTGTTCTGGGGAACTGGACAGATTGGACAACTATAACGACACC
                                                                                                                                                                                                                                     ArgAlaPheLeuProAlaLeuTyrSerLeuLeuPheLeuLeuGlyLeuLeuGlyAsnGly 119
                                                                                                                                                                                                                                                                                                          SerCysCysThrSerProProCysProGln-----AspPheSerLeuAsnPheAsp
                                                                 TCCCTGGTGGAAAATCATCTCTGCCCTGCCACAGAGGGGCCCCTCATGGCCTCCTTCAAG 518
                                                                                                 LeuHisLeuAlaValAlaAspThrLeuLeuValLeuThrLeuProLeuTrpAlaValAsp 159
                                                                                                                                                                                                        GCCGTGTTCGTGCCCGTGGCCTACAGCCTCATCTTCCTCCTGGGCGTGATCGGCAACGTC
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                         COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 mb flo;
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/802,627A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Lee, James
APPLICANT: Wood, William I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1413 TGCCAGCTCTTCCCTAGCTGGCGCAGG---AGCAGTCTCTCTGAGTCAGAGAATGCCACC
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CITY: South San Francisco
STATE: California
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 10-AUG-PRIOR APPLICATION DATA:

10-AUG-1994

08/284586

CLASSIFICATION:

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Best Local Similarity:
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TELEPHONE: 415/225-530
TELEPAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 07/810782
FILING DATE: 19-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NO . .
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LENGTH: 1679 base pairs
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                                                                                              AlaAlaValGlnTrpValPheGlySerGlyLeuCySLysValAlaGlyAlaLeuPheAsn 179
                                                                                                                                                                                                                                                                                                                        LeuHisLeuAlaValAlaAspThrLeuLeuValLeuThrLeuProLeuTrpAlaValAsp 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ArgAlaPheLeuProAlaLeuTyrSerLeuLeuPheLeuLeuGlyLeuLeuGlyAsnGly 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTCGAGAACCTGGAGGACCTGTTCTGGGAACTGGACAGATTGGACAACTATAACGACACC 458
                                 GGGACCATCTGGCTGGGGCTTCCTCCTTGCCTTGCCAGAGATTCTCTTCGCCAAAGTC
                                                                                                                                                                   GTCAACTTCTACTGCAGCAGCCTGCTCCTGGCCTGCATCGCCGTGGACCGCTACCTGGCC 818
                                                                                                                                                                                 IleAsnPheTyrAlaGlyAlaLeuLeuLeuAlaCysIleSerPheAspArgTyrLeuAsn 199
                                                                                                                                                                                                                                  GGCTCTGTGGGCTGGGTCCTGGGGACCTTCCTCTGCAAAACTGTGATTGCCCTGCACAAA 758
                                                                                                                                                                                                                                                                                                    TTCCACCTGGCCGTGGCCGACCTCCTGCTGGTCTTCATCTTGCCCTTTGCCGTGGCCGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LeuGluAsnPheSerSerSerTyr------AspTyrGlyGluAsnGluSerAsp----
---SerAlaHisHisAspGluArgLeuAsnAlaThrHisCysGlnTyrAsnPheProGln 256
                                                              LeuAlaValTrpGlyLeuCysLeuLeuPheAlaLeuProAspPheIlePheLeu-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SerCysCysThrSerProProCysProGln-----AspPheSerLeuAsnPheAsp
                                                                                                                                IleValHisAlaThrGlnLeuTyrArgArgGlyProProAlaArgValThrLeuThrCys 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCCCTGGTGGAAAATCATCTCTGCCCTGCCACAGAGGGGCCCCCTCATGGCCTCCTTCAAG 518
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Matches:
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Indels:
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                                                                                                                                                                                                                                                                                         ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb fl.

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/801,238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                FILING DATE: 19-Feb-
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
                                                                                          APPLICATION NUMBER: 08/0: FILING DATE: 11-JUN-1993 PRIOR APPLICATION DATA: APPLICATION NUMBER: 07/8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Lee, James
APPLICANT: Wood, William
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1113
                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                          FILING DATE: 10-AUG-1994 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: PF4A NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1413 TGCCAGCTCTTCCCTAGCTGGCGCAGG---AGCAGTCTCTCTGAGTCAGAGAATGCCACC 1469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 460 Point San Bru
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     332 AlaLeuAlaArgAsnCysGlyArgGluSerArgValAspValAlaLysSerValThrSer 351
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                NAME: Love, Richard B. REGISTRATION NUMBER: 34,659
                                                                            FILING DATE:
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PheArgGluArgMetTrpMetLeuLeuArgLeuGlyCysProAsnGlnArgGlyLeu 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCCGTGGACAATACCTGCAAGCTGAATGGCTCTCTCCCCGTGGCCATCACCATGTGTGAG 1292
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CAGCGGCGCCCTCAGCGGCAGAAGGCCAGTCAGGGTGGCCATCCTGGTGACAAGCATCTTC 1172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SerArgGlyGlnArgArgLeuArgAlaMetArgLeuValValValValValValAlaPhe 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTCCGCAGTGACCTGTCGCGGCTCCTGACGAAGCTGGGCTGTACCGGCCCTGCCTCCCTG
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19-Feb-1997
                                                                            19-DEC-1991
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RECEPTOR
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/952-9881
TELEPX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1679 base pairs
TYPE: Nucleic Acid
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CAGCGGCGCCTCAGCGGCAGAAGGCAGTCAGGGTGGCCATCCTGGTGACAAGCATCTTC 1172
                         SerArgGlyGlnArgArgLeuArgAlaMetArgLeuValValValValValValAlaphe 311
                                                         CAAGCAGAAACGCATGCCTGGTTCACCTCCCGATTCCTCTACCATGTGGCGGGATTCCTG
                                                                                                                                                                                                                                                                          LeuAlaValTrpGlyLeuCysLeuLeuPheAlaLeuProAspPheIlePheLeu-----
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                                                                                                                                                                                                                                                                                                                                            IleValHisAlaThrGlnLeuTyrArgArgGlyProProAlaArgValThrLeuThrCys 219
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                                                                                                                                                                                          AGCCAAGGCCATCACAACAACTCCCTG-----CCACGTTGCACCTTCTCCCAAGAGAAC
                                                                                                                                                                                                                                                         GGGACCATCTGGCTGGGCTTCCTCCTTGCCTTGCCAGAGATTCTCTTCGCCAAAGTC
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                                                                                                                                                           ValGlyArgThr-----AlaLeuArgValLeuGlnLeuValAlaGlyPheLeu 272
                                                                                                                                                                                                                                                                                                                         ATTGTCCACGCCGTCCATGCCTACCGCCACCGCCGCCTCCTCCCATCACCATCACCTGT 878
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Matches:
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US-08-801-228-5
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                                                                                                                                                 TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: PO
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-530
TELEFAX: 415/952-9881
                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 10-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/0
FILING DATE: 11-JUN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Lee, James
APPLICANT: WOOD, WILLIAM I.
TITLE OF INVENTION: METHODS FOR DETECTION AND AMPLIFICATION
TITLE OF INVENTION: PF4A RECEPTOR NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1293
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                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 1679 base pairs
                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,
                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/6
FILING DATE: 19-DEC-199:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/0 FILING DATE: 19-Feb-1997 CLASSIFICATION: 435
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CITY: South San Francisco
                                                       TOPOLOGY:
                                                                         STRANDEDNESS:
                                                                                         TYPE: Nucleic Acid
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            GlyLeuGlyTyrMetHisCysCysLeuAsnProLeuLeuTyrAlaPheValGlyValLys
TTCCTGGGCCTGGCCTGCTGCCTCAACCCCATGCTCTACACTTTCGCCGGCGTGAAG
                                                                                                                       TTCCTCTGCTGGTCACCCTACCACATCGTCATCTTCCTGGACACCCTGGCGAGGCTGAAG
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                                                                                       AlaLeuAlaArgAsnCysGlyArgGluSerArgValAspValAlaLysSerValThrSer
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                                                          GCCGTGGACAATACCTGCAAGCTGAATGGCTCTCTCCCCGTGGCCATCACCATGTGTGAG
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                                                                                               Query Match:
                                                                                                                 Best Local Similarity:
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                                                                                                                                    Percent Similarity:
                                                                                                                                                                                     Alignment
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Patent No. 6087475
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                     TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/701

FILING DATE: 22-AUG-1996

PRIOR APPLICATION NUMBER: 08/664

FILING DATE: 06-JUN-1996

PRIOR APPLICATION OBTA:

APPLICATION UMBER: 08/076

FILING DATE: 11-JUN-1993

PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: PO
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5530
                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 1679 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 19-DEC-1991 ATTORNEY/AGENT INFORMATION: NAME: Love, Richard B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOCTWARE: WinPatin (Genentech) CURRENT APPLICATION DATA:
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MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy
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                                                                                                                                                                     No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: FILING DATE: 24-Jun CLASSIFICATION:
                 67
                                                                                                                                                                                                                                                                        TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: South San F. STATE: California
                                                                                                                                                                                                                                                       STRANDEDNESS:
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               LeuGluAsnPheSerSerSerTyr--
                                                                                                                                                                                      Scores:
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GENERAL INFORMATION:

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PCT-US94-06380-3
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                                                    TGCCAGCTCTTCCCTAGCTGGCGCAGG----AGCAGTCTCTCTGAGTCAGAGAATGCCACC
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                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alignment Scores:
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: TELEX: 910/371-7168
: INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1679 bases
TYPF:
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NAME: Love, Richard B.
REGISTRATION NUMBER: 34,
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APPLICATION NUMBER:
FILING DATE: 11-JUN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATORY DISRODERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
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                  140 LeuHisLeuAlaValAlaAspThrLeuLeuValLeuThrLeuProLeuTrpAlaValAsp
                                                                                                                                          519
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                                                                                                                                                                                                                                                                                                               67 LeuGluAsnPheSerSerSerTyr------AspTyrGlyGluAsnGluSerAsp---
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TOPOLOGY: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: PCT/US94/06380 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
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TTCCACCTGGCCGTGGCCGACCTCCTGCTGGTCTTCATCTTGCCCCTTTGCCGTGGCCGAG
                                                                                       AlaValAlaAlaValLeuLeuSerArgArgThrAlaLeuSerSerThrAspThrPheLeu
                                                                                                                                          GCCGTGTTCGTGCCCGTGGCCTACAGCCTCATCTTCCTCCTGGGCGTGATCGGCAACGTC
                                                                                                                                                                                                                                                                              CTCGAGAACCTGGAGGACCTGTTCTGGGAACTGGACAGATTGGACAACTATAACGACACC
                                                                     CTGGTGCTGGTGATCCTGGAGCGGCACCGGCAGACACGCAGTTCCACGGAGACCTTCCTG
                                                                                                                                                                       ArgAlaPheLeuProAlaLeuTyrSerLeuLeuPheLeuLeuGlyLeuLeuGlyAsnGly
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K. Jin Kim
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                                                                                                                                                                                                                                  Sequence 8, Application US/08202056 Patent No. 5440021
                                                                                                                                                                                                                      GENERAL INFORMATION:
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch,
COMPUTER: IBM PC compat
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                                                                                                                                     APPLICANT: Kim, Kyung Jin
APPLICANT: Lee, James
TITLE OF INVENTION: Antibodies
NUMBER OF SEQUENCES: 8
                                                                                                                                                                                           APPLICANT: Chuntharapai, Anan APPLICANT: Hebert, Caroline
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                                                                  STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
                                         COUNTRY: US
ZIP: 94080
                                                                                                             ADDRESSEE:
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Best Local Similarity: Query Match:
DB:
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TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: 701
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 29-MAR-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/20
FILING DATE: 25-FEB-1994
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TOPOLOGY: lir
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM:
SOFTWARE: patin (
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Search completed: November 2, 2002, 12:20:16 Job time : 73 secs

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is derived by analysis of the total score distribution.

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ALIGNMENTS

RESULT 1 AAW19780

AAW19780 standard;

Protein;

415 AA

AAW19780;

Human G-protein chemokine receptor HSATU68.

28-SEP-1997 (first entry)

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DNA encoding new isolated human G-protein chemokine receptor - used to develop products for treating, e.g. autoimmune diseases, chronic infections, allergy, malignancy, inflammation or shock
                                                                            Li Y;
                                           WPI; 1997-372810/34.
N-PSDB; AAT72800.
                                                                                                                                                                                                                          HSATU68; G-protein chemokine receptor; 7-transmembrane receptor; signal transduction; therapy; diagnosis; agonist; antagonist; antibody.
                                                                                                                    11-JAN-1996;
                                                                                                                                                                                   W09725340-A1.
                                                                                                (HUMA-) HUMAN GENOME SCI INC
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 29-SEP-1999;
                            28-SEP-2000; 2000WO-US26524
                                                                                     WO200122920-A2
                                                                                                                                              colorectal carcinoma;
                                                                                                                                                          Human; colon cancer; colon cancer antigen;
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Pred. No. 1.2e-236;
0; Mismatches 1;
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Matches 413; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon cancer associated nucleic acid molecules (N) and proteins (P), where the proteins are collectively known as colon cancer antigens. The colon cancer antigens have cytostatic activity and can be used in gene therapy and vaccine production. N and P may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate P expression. For example, N and P may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of P by expressing
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useful f
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                                 NPLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSSWSETSEASYSGL 415
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Pred. No. 6.9e-236;
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and/or treating colorectal
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                                                                                                                                                                                                                        CC This sequence represents human chemokine receptor CXCR3b, a splice CC variant of chemokine receptor CXCR3 (also referred to as CXCR3a). CC Chemokines are a family of small cytokines which bring about the CC chemokines are a family of small cytokines which bring about the CC chemokines are a family of small cytokines which bring about the CC chemokines are less selective. CC all chemokine receptors are seven transmembrane G-protein coupled creceptors and most are receptors for a number of chemokines, CXCR3a being a receptor for the CXC chemokines IP10 and Mig. CXCR3a is CC expressed in activated, but not in resting T-lymphocytes, and may CX cherefore play an important role in the selective recruitment of CX creats which occurs in T-cell mediated inflammatory conditions. CC CXCR3b may have an altered pattern of tissue distribution and CX function in the inflammatory process. Cells expressing the active CXCR3b are useful for identifying ligands, especially agonists and CX antagonists, of a chemokine receptor. In addition, the receptor CXCR3b are useful for interaction with CXCR3b. The modulation CX inflammatory responses is of therapeutic benefit in many conditions CX such as rheumatoid arthritis, psoriasis, multiple sclerosis, atherosclerosis and CX and restranosis.
                                                                                                                                         Query Match
Best Local Similarity
Matches 370; Conserv
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                                                                                                                                                                                          Sequence
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(ASTR ) ASTRA
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156 WAVDAAVQWVFGSGLCKVAGALFNINFYAGALLLACISFDRYLNIVHATQLYRRGPPARV
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                                                                                                                                                                                                                    restenosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         polynucleotide encoding a variant chemokine receptor
                                                                                                  LPGLYTAPSSPFPPSQVSDHQVLNDAEVAALLENFSSSYDYGENESDSCCTSPPCPQDFS
                                                                                       MPGLAHSPGS---PQGWVSDHQVLNDAEVAALLENFSSSYDYGENESDSCCTSPPCPQDFS
                                                  LNEDRAFLPALYSLLFLLGLLGNGAVAAVLLSRRTALSSTDTFLLHLAVADTLLVLTLPL 155
                                    LNFDRAFLPALYSLLFLLGLLGNGAVAAVLLSRRTALSSTDTFLLHLAVADTLLVLTLPL
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                                                                                                                                         Conservative
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                                                                                                                                                   88.7%;
                                                                                                                                      Score 1909; DB 20;
Pred. No. 5.6e-210;
2; Mismatches 6;
                                                                                                                                                               Length
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Вb
WPI; 1998-207381/18
N-PSDB; AAV26557.
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10-SEP-1996;
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                                                              (KOCH-) KOCHER INST THEODOR (LEUK-) LEUKOSITE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCGRESRVDVAKSVTSGLGYMHCCLNPLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          inflammatory disease
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                                                                                                     97US-0829839
96US-0709838
                                                                                                                                           97WO-US15915
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199
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257..27
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127..147
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                                                                                                                                                                                                                                                                                       /note= "N-linked
224..244
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                                                                                                                                                                                                                                                                                                                                                                                                           /note=
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                                                                                                                                                                                                                         "TM7
                                                                                                                                                                                                                                                                                                                                                                                                                                    "N-linked glycosylation site""
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                                    Moser
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RESULT 5
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA encoding CXC chemokine receptor 3 - inhibitors and promoters of which, are useful for treatment of inflammation or in anti-tumour or anti-viral therapy
          13-OCT-1998;
                                  12-OCT-1999;
                                                                                                                                                                                                                                                              AAY90614 standard;
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                                                                                  WO200022129-A1
                                                                                                                                                                                     Human G
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                                                           20-APR-2000
                                                                                                                                               G protein-coupled receptor; GPCR; constitutively active; intracellular loop 3; transmembrane domain 6; drug scree
                                                                                                                                                                                                             21-AUG-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QVSDHQVLNDAEVAALLENFSSSYDYGENESDSCCTSPPCPQDFSLNFDRAFLPALYSLL 110
                                                                                                            sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FLLGLLGNGAVAAVLLSRRTALSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGL 170
                                                                                                                                                                                                                                                                                                                        SYSGL
                                                                                                                                                                                                                                                                                                                                                                                 SGLGYMHCCLNPLLYAFYGYKFRERMMLLLRLGCPNQRGLQRQPSSSRRDSSWSETSEA
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                                                                                                                                                                                                                                                                                                                                                                          SGLGYMHCCLNPLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSSWSETSEA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FLLGLLGNGAVAAVLLSRRTALSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGL 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EVSDHQVLNDAEVAALLENFSSSYDYGENESDSCCTSPPCPQDFSLNFDRAFLPALYSLL 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          364;
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                                                                                                                                                                                     protein-coupled receptor GPR9
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                                                                                                                                     antagonist
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           98US-0170496
                                  99WO-US23938
                                                                                                                                                                                                                                                             Protein;
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99.7%;
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Pred. No. 6.3e-208;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CC of endogenous human orphan (a protesh) coupled receptors (GPCRS, ANY90643-Y90687), and to DNA encoding them (AAA30709-A30743 CC AAY90677) and AAY90683-Y90687), and to DNA encoding them (AAA30709-A30743 CC and AAA30775-A30779). The mutant proteins of the invention contain a CC mutation in a portion of the protein comprising intracellular loop 3 CC (IC3) and transmembrane domain 6 (TM6). A non-endogenous amino acid, X, CC is substituted for an endogenous residue in IC3 at a position 16 amino CC acids N-terminal of an endogenous proline in TM6 to form a sequence CC X-(AA)15-Pro. The endogenous amino acid is selected from Lys, His, Arg CC or Ala, and is preferably Lys. When the endogenous residue at this CC position is Lys, this residue is replaced by His, Arg or preferably Ala. CC The 15 amino acid stretch between the substituted amino acid and the Pro CC may be endogenous, non-endogenous, or a mixture of endogenous and CC mon-endogenous residues. The constitutively active GPCRs are useful for CC identifying antagonists, agonists and partial agonists for use as CC pharmaceutical agents. The mutant proteins are also useful in research constitutions. Antagonists for a particular GPCR are useful for treating diseases and disorders associated with that receptor. Because CC the novel mutant GPCRs are constitutively active, they can be used CC treatily for screening of compounds without the need for endogenous CC ligands. The present sequence represents a human wild-type GPCR referred to in an exemplification of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Non-endogenous constitutively activated human G protein-coupled receptors, useful for identifying agonists for use as pharmaceutical
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                                                                                                                                                                                                                                                                                                                                           CKVAGALENINEYAGALLLACISEDRYLNIVHATQLYRRGPPARVTLTCLAVWGLCLLEA 230
                                     SYSGL
                                                                                                                 SGLGYMHCCLNPLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSSWSETSEA
                                                                                                                                                                             VSRGQRRLRAMRLVVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVT
                                                                                                                                                                                                                                       LPDFIFLSAHHDERLNATHCQYNFPQVGRTALRVLQLVAGFLLPLLVMAYCYAHILAVLL
                                                                                                                                                                                                                                                                                                                      CKVAGALFNINFYAGALLLACISFDRYLNIVHATQLYRRGPPARVTLTCLAVWGLCLLFA
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  SYSGL
                                                                              SGLGYMHCCLNPLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSSWSETSEA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                       415
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99.7%;
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Pred. No. 6.3e-208;
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Best Local Similarity
Matches 364; Conserv
                                                                                                                                                                                                                                                                                                  inflammation), or autolimnue diseases (rheumatold arthritis or lupus), where the (cardio)vascular, lymphatic, respiratory, nervous, digestive, endocrine, motor or urogenital systems or skin are affected, and bone marrow diseases. The products of the invention are chemokine derivatives which have cytostatic, antiinflammatory, antiasthmatic, intiarthritic. Immunosuppressive, dermatological, antirheumatic, antiarthritic. Chemokines act on specific tumor and inflammatory cells through a constellation of chemokine receptors (CR), which control migration and proliferation of these cells. AAG80045-AAG80128 represent human chemokine fragments used to illustrate the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This invention describes a novel diagnostic agent (A) comprising at least two different ligands (I) for receptors (II) that are implicated in disease. (A) are used for the diagnosis of tumors (especially colorectal or prostatic), organ rejection, inflammation and autoimmune diseases. Also inhibitors of (I) are used therapeutically against tumors (and their metastases), inflammation (particularly bronchial asthma or chronic bowel inflammation).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI;
                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 12; 26pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Diagnostic agent containing two or more receptor-specific ligands, useful for detecting tumors, inflammation etc., also therapeutic use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Forssmann W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31-MAR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chemokine; tumour diagnosis; colorectal; prostatic; organ rejection; Inflammation; autoimmune disease; metastasis; bronchial asthma; hupu chronic bowel inflammation; rheumatoid arthritis; cytostatic; antiinflammatory; antiasthmatic; immunosuppressive; dermatological;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human CXCR3 protein.
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                                                                                                   111
                                                                   64
                                                                                                                                                   CKVAGALFNINFYAGALLLACISFDRYLNIVHATQLYRRGPPARVTLTCLAVWGLCLLFA
                CKVAGALFNINEYAGALLLACISFDRYLNIVHATQLYRRGPPARVTLTCLAVWGLCLLFA 230
                                                                                                                                 EVSDHQVLNDAEVAALLENFSSSYDYGENESDSCCTSPPCPQDFSLNFDRAFLPALYSLL
                                                                                                 FLLGLLGNGAVAAVLLSRRTALSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGL 170
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                                                                                                                                                                                                                                                                          368
                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                       87.98;
99.78;
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                                                                                                                                                                                                                       Score 1891; DB 22;
Pred. No. 6.3e-208;
                                                                                                                                                                                                     Mismatches
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RESULT 7
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CC AAY90677 and AAY90683-Y90687), and to DNA encoding them (AAA30709-A30743 CC and AAA30775-A30779). The mutant proteins of the invention contain a mutantion in a portion of the protein comprising intracellular loop 3 CC (IC3) and transmembrane domain 6 (TM6). A non-endogenous amino acid, x, CC is substituted for an endogenous residue in IC3 at a position 16 amino CC acids N-terminal of an endogenous proline in TM6 to form a sequence CC x-(AA)15-Pro. The endogenous amino acid is selected from Lys, His, Arg CC or Ala, and is preferably Lys. When the endogenous residue at this position is Lys, this residue is replaced by His, Arg or preferably Ala. CC The 15 amino acid stretch between the substituted amino acid and the Pro may be endogenous, non-endogenous, or a mixture of endogenous and con-endogenous residues. The constitutively active GPCRs are useful for identifying antagonists, agonists and partial agonists for use as C pharmaceutical agents. The mutant proteins are also useful in research settings for elucidating the roles of the receptors in normal and cc diseased conditions. Antagonists for a particular GPCR are useful for
                                                                                                                                                                                                                                                                                         The invention relates to constitutively active, non-endogenous versions of endogenous human orphan G protein-coupled receptors (GPCRs, AAY90643-AAY90677 and AAY90683-Y90687), and to DNA encoding them (AAA30709-A30743
                                                                                                                                                                                                                                                                                                                                                                                                      agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            G protein-coupled receptor; GPCR; constitutively active; intracellular loop 3; transmembrane domain 6; drug scree
                                                                                                                                                                                                                                                                                                                                                                     Example
                                                                                                                                                                                                                                                                                                                                                                                                                      Non-endogenous constitutively activated human G protein-coupled receptors, useful for identifying agonists for use as pharmaceu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Behan DP,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (AREN-) ARENA PHARM INC
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t; mutant; mutein.
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            Gorman DM,
Zlotnik A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the novel mutant GPCRs are constitutively active, they can be used directly for screening of compounds without the need for endogenous ligands. Sequences ANY90643- ANY90677 and ANY90683-Y90687 the mutant human GPCRs of the invention.
                                                                            23-JAN-1997;
                                                                                                                                                                                                                                                                                                                                                                                        AAW69999 standard;
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                                                                                                        22-JAN-1998;
                                                                                                                                                            WO9832858-A2
                                                                                                                                                                                                                          inflammatory response: immune response; leukocyte migration; GPCR; leukocyte adhesion; chemoattractant; modulation; antivital response; cellular morphology modification response; G-protein coupled receptor; phosphoinositide lipid turnover; abnormal proliferation; regeneration;
                                                                                                                                                                                                                                                                              Chemokine; primate; human; rodent; chemokine receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   treating diseases and disorders associated with that receptor. Because the novel mutant GPCRs are constitutively active, they can be used
                                                  (SCHE ) SCHERING
                                                                                                                                 30-JUL-1998
                                                                                                                                                                                                                                                                                                          Rodent chemokine receptor HST01.1 amino acid sequence
                                                                                                                                                                                                                                                                                                                                      20-OCT-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SGLGYMHCCLNPLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSSWSETSEA 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LPDFIFLSAHHDERLNATHCQYNFPQVGRTALRVLQLVAGFLLPLLVMAYCYAHILAVLL 290
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FLLGLLGNGAVAAVLLSRRTALSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGL 170
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                         Hedrick JA,
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                                                                                                       98WO-US00902
                                                                                                                                                                                                                                                                                                                                                                                        Protein; 367
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99.5%;
                         Mattson JD,
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Pred. No. 3
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                         Soto-trejo
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3.1e-207;
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CC therapeutically to treat conditions associated with abhormal physiology
CC or development e.g. inflammatory conditions such as asthma. Chemokines
CC are important in immune and inflammatory responses in that they induce
CC leukocyte migration and adhesion. They are also chemoattractants for
CC several cells involved in inflammation and can induce other biological
CC responses e.g. modulation of second messenger levels (e.g. Ca++),
CC cellular morphology modification responses, phosphinositide lipid
CC turnover, possible antiviral responses etc. The chemokine receptors of
CC the invention exhibit structural properties of G-protein coupled
CC receptors (GPCR), although their ligands have not yet been identified.
CC ligand: receptor complexes in vivo or in assay techniques. Assays may
CC also involve chemical antagonists which block complex production or
CC (especially neurons, macrophages or lymphocytes) to treat e.g. abnormal
CC (especially neurons, macrophages or lymphocytes) to treat e.g. abnormal
CC (especially neurons, macrophages or lymphocytes) to treat e.g. abnormal
CC are also used to produce antibodies useful diagnostically, for drug
CC screening or for polypeptide purification. The polypeptides are useful
CC polypeptides or related sequences, especially from other species. They
CC also allow transformation of cells for polypeptides. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This represents a rodent chemokine receptor HST01.1 amino acid sequence. The invention provides novel primate and rodent chemokines and chemokine receptors. The chemokines, receptors and binding compounds (optionally antibodies/fragments specifically binding the chemokines) are useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rodent and primate chemokines and chemokine receptors - useful diagnostically and therapeutically to treat conditions associated with abnormal physiology or development e.g. inflammatory conditions \frac{1}{2} \left( \frac{1}{2} \right) \left( \frac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim
Sequence
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       367 AA;
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Query Match Best Local Matches 363 411 303 351 243 183 123 171 111 291 231 63 CKVAGALFNINFYAGALLLACISFDRYLNIVHATQLYRRGPPARVTLTCLAVWGLCLLFA 230 QVSDHQVLNDAEVAALLENFSSSYDYGENESDSCCTSPPCPQDFSLNFDRAFLPALYSLL 110 SYLGL SYSGL SGLGYMHCCLNPLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSSWSETSEA VSRGQRRFRAMRLVVVVVAAFAVCWTPYHLVVLVDILMDVGVLARNCGRKSHVDVAKSVT VSRGQRRLRAMRLVVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVT LPDFIFLSAHHDERLNATHCQYNFPQVGRTALRVLQLVAGFLLPLLVMAYCYAHILAVLL 290 EVSERQVLDASDFAFLLENSTSPYDYGENESD~FSDSPPCPQDFSLNFDRTFLPALYSLL 62 SGMGYMHCCLNPLLYAFVGVKFREKMWMLFTRLGRSDQRGPQRQPSSSRRESSWSETTEA LPDFIYLSANYDQRLNATHCQYNFPQVGRTALRVLQLVAGFLLPLLVMAYCYAHILAVLL 314; Similarity 367 Conservative 75.6%; 86.0%; 22; Score 1626.5; Pred. No. 1.4e Mismatches 1.4e-177; 28; Indels 1: Gaps 182 302 350 242 ۲;

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                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                     (BLC, see AAY06641). The methods comprise combining BLR1 and BLC polypeptides with a candidate modulator agent under conditions whereby, but for the presence of the agent, the polypeptides engage in a first interaction, and determining a second interaction of the polypeptides in the presence of the agent, wherein a difference between the first and second interactions indicates that the agent modulates the interaction of the polypeptides. The modulator is preferably an antagonist, especially dominant negative, form of BLC. BLC and BLC agonists and antagonists may be useful for treating viral (e.g. HIV) infections, lymphoma, B lineage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Burkitt's lymphoma receptor 1; BLR1; mouse; B lymphocyte chemoattractant; BLC; chemokine; ligand; drug screening; leukaemia; autoimmune disease; therap
                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                           thyroiditis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    interaction of BLR1 with its ligand, B lymphocyte chemoattractant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence represents mouse Burkitt's lymphoma receptor 1 (BLR1). The invention relates to methods for modulating the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 35; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Modulating interaction of a Burkitt's Lymphoma Receptor 1 polypeptide and ligand, useful in drug screens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cyster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-JUN-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9928468-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mouse Burkitt's lymphoma receptor 1 (BLR1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY06643;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY06643 standard; Protein;
   302
                                                                                                  143
                                                                                                                                                                                                 130
                                                                                                                                                                                                                                                                                                                                                                                                           eukaemia, and autoimmune diseases such as rheumatoid arthritis
                                   202
                                                                                                                                  190
                                                                                                                                                                 83
                                                                                                                                                                                                                               26
                                                                                                                                                                                                                                                              70
                                                                                                                                                                                                                                                                                              Local Similarity es 143; Conserv
                                                                                                                                                                                TALSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGLCKVAGALFNINFYAGALLL 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1999-493764/41.
DB; AAX87709.
RLVVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVTSGLGYMHCCLN 361
                                                 ATHCQYNFPQVGRT----ALRVLQLVAGFLLPLLVMAYCYAHILAVLL-VSRGQRRLRAM 301
                                                                                                                             ACISFDRYLNIVHATQLYRRGPPARVTLTCLAVWGLCLLFALPDFIFLSA---HHDERLN 246
                                                                                                                                                             HTRSSTETFLFHLAVADLLLVFILPFAVAEGSVGWVLGTFLCKTVIALHKINFYCSSLLV 142
                                                                                                                                                                                                                                                          FSSSYDYGENESDSCCTSPPCPQDFSLNFDRAFLPALYSLLFLLGLLGNGAVAAVLLSRR 129
                                -PQCTFSQENEAETRAWFTSRFLYHIGGFLLPMLVMGWCYVGVVHRLLQAQRRPQRQKAV
                                                                                              ACIAVDRYLAIVHAVHAYRRRRLLSIHITCTAIWLAGFLFALPELLFAKVGQPHNNDSL- 201
                                                                                                                                                                                                                              YSNSTEIPLQDSNFCST---VEGPLLTSFKAVFMPVAYSLIFLLGMMGNILVLVILERHR 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ,
5
                                                                                                                                                                                                                                                                                                                                                             374 AA;
                                                                                                                                                                                                                                                                                                                                                                                             and diabetes.
                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97US-0982493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98WO-US25561
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                                                                                                                                                                                                                                                                                                            29.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Williams LT;
                                                                                                                                                                                                                                                                                           %; Score 640; DB 20;%; Pred. No. 2.4e-64;54; Mismatches 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        374 AA
                                                                                                                                                                                                                                                                                            139;
                                                                                                                                                                                                                                                                                                                         Length 374;
                                                                                                                                                                                                                                                                                           Indels 14;
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RESULT 10
ABG13609
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                                                             CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC and gene mapping, and in recombinant production of (II). The CC polynucleotides are also used in diagnostics as expressed sequence tags CC for identifying expressed genes. (I) is useful in gene therapy techniques (II). (II) is useful for generating antibodies against it, detecting or CC (II). (II) is useful for generating antibodies against it, detecting or CC quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical climaging of sites expressing (II). (I) and (II) are useful for treating CC imaging of sites expressing (II). (I) and (II) are useful for treating CC disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in CC diagnostics, forensics, gene mapping, identification of mutations cresponsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and CC amino acid sequences. ABG00010-ABG30377 represent novel human CC specification, but was obtained in electronic format directly from WIPO case of the content of the printed content of the content of the printed content of the content of the content of the printed content of the conten
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity -
  Sequence
                                              at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to isolated polynucleotide (I) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 20; SEQ ID No 43968; 103pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-639362/73
N-PSDB; AAS77796.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31-MAR-2000;
23-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; chromosome mapping; gene mapping; gene therapy; forensic
food supplement; medical imaging; diagnostic; genetic disorder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABG13609 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 polypeptide (II) sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-MAR-2001; 2001WO-US08631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200175067-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel human diagnostic protein #13600
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABG13609;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       321
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSSWSETSEAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      399 AA;
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2000US-0649167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (I) is useful as hybridisation probes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        411
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Query Match
Best Local Similarity
Matches 154; Conserv

29.6%; illarity 37.3%; Conservative !

57;

Score 637.5; DB 22, Pred. No. 5.2e-64; 7; Mismatches 145;

Indels Length

Gaps

10;

DB 22;

399; 57;

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            \begin{array}{l} \mathbf{p} \times \mathbf
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; cytokine; cell proliferation; cell differentiation; growth factor; haematopoiesis regulation; tissue growth; immunomodulator; activin; inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis; proliferation; metastasis; cancer; tumour; haematopoietic disorder; myeloid cell disorder; lymphoid cell disorder; asthma; arthritis; chronic inflammatory condition; proliferative retinopathy; atheroscierosis; coronary heart disease; arterial ischaemia; bone disorder; osteoporosis; vascular growth disorder; tissue regeneration; wound healing; infection; immune disorder;
                                                                                                                                                                                                                                                                                         Tang
Human proteins and DNA encoding sequences useful for
                                                                                                                     N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 03-FEB-2000;
27-APR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-FEB-2001; 2001WO-US03800
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tissue regeneration; wound healing; infection; immune disorde cell culture; drug screening; gene therapy; antiinflammatory; antiasthmatic; antiarthritic; haemostatic; antiarteriosclerot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human IL-8R B homologue, SEQ ID NO:2394.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-JAN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                  (HYSE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antitungal; vulnerary; antiulcer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cytostatic; osteopathic; vasotropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       178
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                                                                                                                                                                                     2001-457740/49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGVLQVKS-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SSNVSPA-C---YEDMGNNTANWRMLLRILPQSFGFIVPLLIMLFCYGFTLRTLFKAHMG
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                                                                                                                                                                                                                                                                                                                                                                                                        HYSEQ INC
                                                                                                                          ABA09268
                                                                                                                                                                                                                                                                                         Liu C,
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2000US-0560875
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ant; virucide; antibac
preventing
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treating or ameliorating a medical condition in a mammalian subject \ensuremath{\text{e.g.}} arthritis and cancer -
                                                                                                        English
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Componential therapeutic applications. The polypeptides of the invention may differentiation activities, including cytokine, cell proliferation or cell differentiation activities; stem cell growth factor activity; cell immunomodulatory activities; stem cell growth factor activity; cell immunomodulatory activity; activin- or inhibin-related activities; chaematopoiesis regulatory activity; tissue growth activities; cor chamotractic or chemokinetic activities; haematotatic, thrombotic or thrombolytic activities; activities; haematotatic, thrombotic or chemokinetic activities; provides and nucleotides of the invention are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Such conditions include cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell conditions, e.g., by protein or gene therapy. Such conditions include carterial ischaemia, bone disorders (e.g., myeloid or lymphoid cell vascular growth. Polypeptides involved with tissue regeneration and carterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal carterial ischaemia or uncisions and ulcers), while those with carterial ischaemia or viral, communicativities may be used to promote with the can be used to use invention also relates to vectors and recombinant host cells comprising a nucleotide of the invention, methods of producing the novel polypeptides, antibodies against the polypeptides, methods of detecting the nucleotides or polypeptides in a sample, and methods of identifying compounds which bind to polypeptides of the invention. Honough novel, many of the polypeptides of the invention have homology to known proteins, thereby giving an insight into their probable biological activities, and hence polypeptide Sequences ABB10981-ABB12330 techniques. The present sequence represents a novel human ABA08225-ABA09574 of the invention represent 1350 novel human polypeptides, and are acids encoding them. The and

Sequence 399 AA;

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QKHRAMRVIFAVVLIFLLCWLPYNLVLLADTLMRTQVIQETCERRNHIDRALDATEILGI 343
                              RRLRAMRLVVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVTSGLGY 355
                                                                                                                                                    CISFDRYLNIVHATQLYRRGPPARVTLT------CLAVWGLCLLFALPDFIFLSAHH
                                                                                                                                                                                                GRSVTDVYLLNLALADLLFALTLPIWAASKVNGWIFGTFLCKVVSLLKEVNFYSGILLLA 177
                                                                                                                                                                                                                                                                                            SSSYDYGENESDSCCTSPPCPQDFSLNFDRAFLPALYSLLFLLGLLGNGAVAAVLLSRRT 130
                                                                                                                                                                                                                                                                                                                                                               GGAAQSKSQTKSDSITKEFLPGLYTAPSSPFP-PSQVSDHQVLNDAEVAALLENF-----
                                                               SSNVSPA-C---YEDMGNNTANWRMLLRILPQSFGFIVPLLIMLFCYGFTLRTLFKAHMG
                                                                                              DERLNATHCQYNFPQVG-----RTALRVLQLVAGFLLPLLVMAYCYAHILAVLLVSRGQ
                                                                                                                                 CISVDRYLAIVHATR ---
                                                                                                                                                                                                                               ALSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGLCKVAGALFNINFYAGALLLA 190
                                                                                                                                                                                                                                                              LSNYSYSSTLPPFLLDAAPCEPE-SLEINKYFVVIIYALVFLLSLLGNSLVMLVILYSRV 117
                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                 29.6%;
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                                                                                                                               --TLTQKRYLVKFICLSIWGLSLLLALPVLLFRRTVY
                                                                                                                                                                                                                                                                                                                                                                                                               Score 637.5;
Pred. No. 5.
                                                                                                                                                                                                                                                                                                                                  -PATQSGFKFTSKMEDFNMESDS----FEDFWKGED
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                                                                                                                                                                                                                                                                                                                                                                                                                                DB 22; Length 399;
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MHCCLNPLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSSWSETS

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                                                                                                                                                                                                Query Match
Best Local S
Matches 147
                                                                                                                                                                                                                                                                       The II-8 receptor cDNA sequence was isolated (see AAQ29505) and a 874bp sub-fragment of the coding sequence was used as a probe to screen human cell line HL60 and human peripheral blood lymphocyte cDNA libraries. Two new gene sequences were found that are clearly related to the II-8 receptor. One of these was contained in clone 8rr.9 and 1s predicted to encode an amino acid sequence which is 56% and 38% identical with the high and low affinity II-8 receptor sequences, respectively. See also AAQ37107.
                                                                                                                                                                                                                                                                                                                                                                                        Claim 7;
                                                                                                                                                                                                                                                                                                                                                                                                               Isolated human platelet factor 4 super-family receptor polypeptide and corresp. antibodies and DNA - useful as diagnostic and screening agents, and for treating inflammation PF4AR-mediated disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-MAR-1991;
19-DEC-1991;
                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1992-366191/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pro-inflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR27793;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-MAR-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New platelet factor 4 receptor superfamily member PF4ARii
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             -SAHHDERLNATHCQYNFPQVGRT----ALRVLQLVAGFLLPLLVMAYCYAHILAVL-LV
                                              VNFYCSSLLLACIAVDRYLAIVHAVHAYRHRRLLSIHITCGTIWLVGFLLALPEILFAKV
                                                              INFYAGALLLACISFDRYLNIVHATQLYRRGPPARVTLTCLAVWGLCLLFALPDFIFL---
                                                                                                 LVLVILERHRQTRSSTETFLFHLAVADLLLVFILPFAVAEGSVGWVLGTFLCKTVIALHK 130
                                                                                                              LENLEDLFWELDRLDNYNDTSLVENHLCPATEGPLMASFKAVFVPVAYSLIFLLGVIGNV 70
                                                                                                                                                                          LENFSSSY---DYGENESD-SCCTSPPCPQ---DFSLNFDRAFLPALYSLLFLLGLLGNG 119
                                                                                                                                                                                                   al Similarity
147; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      G-protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAQ37107.
                                                                                                                                                                                                                                                                                                                                                                                       Fig 5; 78pp; English.
                                                                                                                                                                                                                                                    372
                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lee J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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91US-0810782
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        coupled receptor family; rhodopsin superfamily;
cytokine; 8rr.9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wood
                                                                                                                                                                                                            29.5%;
                                                                                                                                                                                                   50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        372
                                                                                                                                                                                                Score 635; DB 1
Pred. No. 9e-64;
0; Mismatches 1
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                                                                                                                                                                                                                         DB 13; Length 372;
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LENLEDLFWELDRLDNYNDTSLVENHLCPATEGPLMASFKAVFVPVAYSLIFLLGVIGNV LENFSSSY----DYGENESD-SCCTSPPCPQ----DFSLNFDRAFLPALYSLLFLLGLLGNG 119

50;

145;

Indels

18;

Gaps

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RESULT 13
AAR92239
ID AAR92
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Query Match
Best Local Similarity 40.8
Matches 147; Conservative
                                                                    to treat or prevent inflammation e.g. psoriasis, dermatitis, rheumatoid arthritis and particularly inflammatory bowel disease and chronic lung inflammation. When immobilised, these antibodies may be used to detect interleukin-8 receptor B expression in cells and tissues and for affinity purification of interleukin-8 receptor B from cells. This sequence is an additional chemokine superfamily receptor which was identified by probing lamda libraries of genomic DNA from a human monocyte-like cell line (L-60) and human peripheral blood lymphocytes using a large fragment of the interleukin-8 type A receptor DNA (See AAQ99006).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Interleukin; IL-8; inflammation; psoriasis; dermatitis;
rheumatoid arthritis; inflammatory bowel disease;
chronic lung inflammation; treatment; antibody;
                                                 Sequence
                                                                                                                                                                                                                    Example 2; Columns 49-52; 62pp; English.
                                                                                                                                                                                                                                                        New antibodies against interleukin 8 type B or prevent inflammation, also for detecting
                                                                                                                                                                                                                                                                                                                                                       (KIMK/)
                                                                                                                                                                                                                                                                                                                                                                                                                  25-FEB-1994;
29-MAR-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chemok ine
                                                                                                                                                                                             Antibodies directed
                                                                                                                                                                                                                                                                                            N-PSDB;
                                                                                                                                                                                                                                                                                                         WPI;
                                                                                                                                                                                                                                                                                                                               Chuntharapai A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-MAR-1991;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US5440021-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   affinity purification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR92239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR92239 standard; Protein; 372 AA
                                                                                                                                                                                                                                                                                                                                                                                           (CHUN/) CHUNTHARAPAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                (HEBE/)
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                                                                                                                                                                                                                                                                                                                                                        KIM K J.
LEE J.
                                                                                                                                                                                                                                                                                           AAQ99009
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                superfamily
                                                 372
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                                                 AA;
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91US-0677211
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                                                                                                                                                                                             against the interleukin-8 receptor
            29.5%;
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Mismatches
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           1635; DB 16
No. 9e-64;
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                      16;
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RESULT 14
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 Query Match
Best Local Similarity
Matches 147; Conserv
                                                                         2 PF4AR members were identified by probing lambda libraries from human monoclyte-like cell line HL-60 and human peripheral blood lymphocytes using a large fragment of IL-8 receptor DNA (full sequence given in AAQ80520). The nucleotide sequences of the 2 PF4ARs are given in AAQ80521 and AAQ80522, and their respective amino acid sequences in AAR68812 and AAR68813.
                                                     Sequence
                                                                                                                                                                                                          Treatment of inflammatory disorders - by administering an antibody capable of binding a platelet factor 4 superfamily
                                                                                                                                                                                                                                                       N-PSDB; AAQ80522
                                                                                                                                                                                                                                                                                          Chuntharapai A,
                                                                                                                                                                                                                                                                                                                                              11-JUN-1993;
                                                                                                                                                                                                                                                                                                                                                                        07-JUN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Interleukin-8 receptor; IL-8 receptor; PF4AR; platelet factor superfamily receptor; lymphocyte; chemotactic; inflammation; inflammation; disease; arthritis; emphysema; cystfibrosis; colitis; bronchitis; meningitis; therapeutic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-JUL-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR68813 standard; Protein; 372
                                                                                                                                                                                                                                                                                                                    (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                    22-DEC-1994
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                                                                                                                                                                                                                                                                   1995-036114/05
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QRRPQRQKAVRVAILVTSIFFLCWSPYHIVIFLDTLARLKAVDNTCKLNGSLPVAITMCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -SAHHDERLNATHCQYNFPQVGRT----ALRVLQLVAGFLLPLLVMAYCYAHILAVL-LV
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                                                   372
                                                                                                                                                                        Page 56-58;
  Conservative
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                                                   ΑĄ;
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                                                                                                                                                                                                                                                                                             Hebert
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            29.5%;
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            Score 635; DB 1
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Indels
18;
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         This sequence represents human Burkitt's lymphoma receptor 1 (BLR1). The invention relates to methods for modulating the interaction of BLR1 with its ligand, B lymphocyte chemoattractant (BLC, see AAY06642). The methods comprise combining BLR1 and BLC polypeptides with a candidate modulator agent under conditions whereby, but for the presence of the agent, the polypeptides engage in a first interaction, and determining a second interaction of the polypeptides in the presence of the agent, wherein a difference between the first and second interactions indicates that the agent modulates the interaction of the polypeptides. The modulator is preferably an anasonist, especially dominant negative, form of
                                                                                                                                                                                                                                                                                                           Cyster
                                                                                                                                                                                                                  Modulating interaction of a Burkitt's Lymphoma Receptor polypeptide and ligand, useful in drug screens
                                                                                                                                                                                                                                                                               WPI; 1999-493764/41.
                                                                                                                                                                                                                                                                                                                                                                     02-DEC-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  drug
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Burkitt's lymphoma receptor 1; BLR1; human;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               lymphocyte chemoattractant; BLC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  screening;
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                                                                                                                                                                                                                                                                                                           JG,
                                                                                                                                                                                        Page 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               standard;
                                                                                                                                                                                                                                                                                                           Gunn MD,
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                                                                                                                                                                                                                                                                                                                                                                                                98WO-US25561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  leukaemia; autoimmune disease;
                                                                                                                                                                                       42pp;
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                                                                                                                                                                                                                                                                                                           Williams
                                                                                                                                                                                       English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               chemokine; ligand;
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useful
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                                                                                                                                                                                                                                                                                                                                                                                                                  treating viral (e.g. HIV) infections, lymphoma, B lineage leukaemia, and autoimmune diseases such as rheumatoid arthritis, thyroiditis and diabetes.
                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                            131 VNFYCSSLLLACIAVDRYLAIVHAVHAYRHRRLLSIHITCGTIWLVGFLLALPEILFAKV 190
                                                                                                                                                                                                                                          180 INFYAGALLLACISFDRYLNIVHATQLYRRGPPARVTLTCLAVWGLCLLFALPDFIFL-- 237
                                                                                                                                                                                                                                                                                          11 LENLEDLFWELDRLDNYNDTSLVENHLCPATEGPLMASFKAVFVPVAYSLIFLLGVIGNV 70
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                                                                                                                                                                                                                                                                                                                                                                                            372 AA;
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Title:
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      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
1629.5
641
640
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2: pir2:*
3: pir3:*
4: pir4:*
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Match
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   2, 2002, 12:05:20 ; Search time 44 Seconds (without alignments)
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                  G protein-coupled G protein-coupled G protein-coupled G protein-coupled interleukin-8 rece interleukin-9 rece lymphocyte-specifi fusin (LESTRA) - c neuropeptide Y/pep interleukin-8 rece neuropeptide Y/pep G protein-coupled C protein-coupled C protein-coupled C protein-coupled C protein-coupled Chemokine (C-C) re chemokine (C-C) re chemokine (C-C) re chemokine (C-C) re macrophage inflamm G protein-coupled Chemokine (C-C) re macrophage inflamm G protein-coupled C protein-c 
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probable G
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C;Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 21-Jul-2000
C;Accession: JE0349
R;Tamaru, M; Tominaga, Y; Yatsunami, K; Narumi, S.
Biochem. Biophys. Res. Commun. 251, 41-48, 1998
A;Title: Cloning of the murine interferon-inducible protein 10 (IP-10) receptor A;Reference number: JE0349; MUID:99009219
A;Accession: JE0349
A;Accession: JE0349
A;Molecule type: mRNA
A;Residues: 1-367 <TAM>
A;Residues: 1-367 <TAM>
A;Residues: 1-367 <TAM>
A;Comment: This protein is important for lymphocyte trafficking to lymphoid org
RESULT
S32785
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45	44	43	42	41	40	39	38	37	36	ω 5	34	ω u	32	31	30
447	447.5	452	453	454	456.5	458.5	458.5	461	464.5	470.5	471.5	473.5	484	491.5	492
20.8	20.8	21.0	21.1	21.1	21.2	21.3	21.3	21.4	21.6	21.9	21.9	22.0	22.5	22.8	22.9
362	359	362	359	359	359	359	359	359	355	359	359	359	383	355	359
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A30341	139418	A39714	JC1194	A48857	S44425	JC2134	JH0621	JC1104	JC4304	A42656	JQ1516	S15403	S55594	G02436	I49341
G protein-coupled	angiotensin II rec	G protein-coupled	angiotensin II rec	angiotensin II rec	2	angiotensin II rec	angiotensin II rec	angiotensin II rec	orphan G protein-c	angiotensin II rec	angiotensin II rec	angiotensin II rec	G protein-coupled	chemokine (C-C) re	MIP-1 alpha recept

ALIGNMENTS

mouse

(IP-10) receptor

to lymphoid organs

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Query Match 75.8%;
Best Local Similarity 86.3%;
Matches 315; Conservative 21
363
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                                                                                                                                                                                                                                   CKVAGALFNINFYAGALLLACISFDRYLNIVHATQLYRRGPPARVTLTCLAVWGLCLLFA 230
                                                                                                                                                                                                                                                                         FLLGLLGNGAVAAVLLSQRTALSSTDTFLLHLAVADVLLVLTLPLWAVDAAVQWVFGPGL 122
SYLGL
                                                                                                                                                                                                                      CKVAGALFNINFYAGAFLLACISFDRYLSIVHATQIYRRDPRVRVALTCIVVWGLCLLFA 182
                        SYSGL 415
                                                                                                                                                               LPDFTYLSANYDQRLNATHCQYNFPQVGRTALRVLQLVAGFLLPLLVMAYCYAHILAVLL
367
                                                                                                                                                                                                                                                                                                                                                                                     %; Score 1629.5; DB 2;
%; Pred. No. 4e-136;
21; Mismatches 28;
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A;Cross-references: GB:L20332; NID:g438798; PIDN:AAA16852.1; PID:g438799 C;Superfamily: vertebrate rhodopsin C;Keywords: G protein-coupled receptor; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 3
$42628

G protein-coupled receptor Gpcr6 - mouse

G protein-coupled receptor Gpcr6 - mouse

N;Alternate names: interleukin-8 receptor homolog; muBLR1 protein

C;Species: Mus musculus (house mouse)

C;Date: 07-Sep-1994 #sequence_revision 26-May-1995 #text_change 2:
                                                                                                                                                       A;Cross-references: EMBL:X71788; NID:g2598563; PIDN:CAA50673.1; PID:g433947 R;Wilkle, T.M.; Chen, Y.; Gilbert, D.J.; Moore, K.J.; Yu, L.; Simon, M.I.; (Genomics 18, 175-184, 1993 A;Title: Identification, chromosomal location, and genome organization of mah;Reference number: A48909; MUID:94116980 A;Accession: C48909
                                                                                                                                                                                                                                                                                                                                    A; Title: The G protein-coupled receptor BLR1 A; Reference number: S42628; MUID:94009211 A; Accession: S42628
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A; Residues: 1-374 < KOU>
                                                                                                A; Molecule type: mRNA
A; Residues: 151-269 <WIL>
                                                                                                                                     A; Status: preliminary; nucleic acid sequence
                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-374 <KAI>
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                                                                                                                                                                                                                                                                                                                A; Status: preliminary; nucleic acid sequence not shown
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Best Local Similarity 4...
146; Conservative
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  Query
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J. Immunol. 23, 2532-2539, 1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HTRSSTETFLFHLAVADLLLVFILPFAVAEGSVGWVLGTFLCKTVIALHKINFYCSSLLL 142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RLVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVTSGLGYMHCCLN 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -PQCIFSQENEAETRAWFASRFLYHTGGFLLPMLVMAWCYVGVVHRLLQAQRRPQRQKAV
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41.7%; Pr
tive 50;
    29
                                      receptor; transmembrane protein
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Pred. No. 8.1e-49;
50; Mismatches 140
  Score
640;
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  DВ
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Length 374;
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R;Dobner, T.; Wolf, I.; Emrich, T.; Lipp, M. Eur. J. Immunol. 22, 2795-2799, 1992
A;Title: Differentiation-specific expression A;Reference number: $26667; MUID:93049615
A;Accession: $26667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 4
236667
G protein-coupled receptor BLR1 - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995
C;Accession: 826667
C;Accession: 826667
                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GDB:136235; OMI
A;Map position: 15q26.1-15q26.1
C;Superfamily: vertebrate rhdopsin
C;Keywords: G protein-coupled recept
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δÃ
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A; Residues: 1-372 < DOB>
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Best Local S
Matches 147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACISFDRYLNIVHATQLYRRGPPARVTLTCLAVWGLCLLFALPDFIFLSA---HHDERLN 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TALSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGLCKVAGALFNINFYAGALLL 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YSNSTEIPLQDSNFCST---VEGPLLTSFKAVFMPVAYSLIFLLGMMGNILVLVILERHR 82
QRRPQRQKAVRVAILVTSIFFLCWSPYHIVIFLDTLARLKAVDNTCKLNGSLPVAITMCE 308
                                  SRGQRRLRAMRLYVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVTS
                                                                       SQGHHNNSL--PRCTFSQENQAETHAWFTSRFLYHVAGFLLPMLVMGWCYVGVVHRLRQA
                                                                                                                                                VNFYCSSLLLACIAVDRYLAIVHAVHAYRHRRLLSIHITCGTIWLVGFLLALPEILFAKV 190
                                                                                                                                                                   INFYAGALLLACISFDRYLNIVHATQLYRRGPPARVTLTCLAVWGLCLLFALPDFIFL---
                                                                                                                                                                                                                       LVLVILERHRQTRSSTETFLFHLAVADLLLVFILPFAVAEGSVGWVLGTFLCKTVIALHK 130
                                                                                                                                                                                                                                          AVAAVLLSRTALSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGLCKVAGALFN 179
                                                                                                                                                                                                                                                                                              LENLEDLFWELDRLDNYNDTSLVENHLCPATEGPLMASFKAVFVPVAYSLIFLLGVIGNV 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PMLYTFAGVKFRSDLSRLLTKLGCAGPASL-CQLFPNWRKSSLSESENAT
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                                                                                          -SAHHDERLNATHCQYNEPQVGRT----ALRVLQLVAGFLLPLLVMAYCYAHILAVL-LV
                                                                                                                                                                                                                                                                                                                                 LENFSSSY----DYGENESD-SCCTSPPCPQ----DFSLNFDRAFLPALYSLLFLLGLLGNG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSSWSETSEAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        - PQCTFSQENEAETRAWFTSRFLYHIGGFLLPMLVMGWCYVGVVHRLLQAQRRPQRQKAV
                                                                                                                                                                                                                                                                                                                                                                       al Similarity
147; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                              protein-coupled receptor; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                       Conservative
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4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                    Score 635; DB 2;
Pred. No. 2.7e-48;
                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9.9e-49;
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A;Cross-references: EMBL:U11872; NID:g511808; PIDN:7
11876; NID:g511816; PID:g511817; EMBL:U11877; NID:g5
R:Sprenger, H.; Lloyd, A.R.; Lautens, L.L.; Bonner,
J. Biol. Chem. 269, 11065-11072, 1994
A;Title: Structure, genomic organization, and express
A;Reference number: A53611; MUID:94209273
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Homo sapiens (man)
C;Date: 07-Oct-1994 #sequence_revision 12-Apr-1996 #text_change
C;Accession: 137898; 138712; A55611; A39446
R;Ahuja, S.K.; Shetty, A.; Tiffany, H.L.; Murphy, P.M.
J Biol. Chem. 269, 26381-26389, 1994
A;Title: Comparison of the genomic organization and promoter fun A;Reference number: 137898; MUID:95014476
A;Accession: 137898
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A;Cross references: GDB:127868; OMIM:146928
A;Map position: 2q35-2q35
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; tra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:M99412; GB:L19593
R;Murphy, P.M.; Tiffany, H.L.
Science 253, 1280-1283, 1991
A;Title: Cloning of complementary DNA encoding a A;Reference number: A39446; MUID:91368200
A;Accession: A39446
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C;Comment: This receptor, unl
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A;Accession: I38712
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A; Residues: 6-360 < MUR>
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A; Residues: 6-360 <SPR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-15 <RE2>
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                                                                                                                                                                                                                                                                                                                                                                           Matches
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                                                                                                                                                                                                                                                                                                                               72
                                                                                                                                                                                                                                                                                                                                                                                                Match 29.4%; Score 633; DB 2; Local Similarity 40.1%; Pred. No. 3.9e-48;
                                                                                                                                                                                                               LSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGLCKVAGALFNINFYAGALLLAC 191
                                                                                                                                                                                                                                                                                                                          SSYDYGENESDSCCTSPPCPQDFSLNFDRAFLPALYSLLFLLGLLGNGAVAAVLLSRRTA 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GLGYMHCCLNPLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSSRRDSSWSETSEAS
SNVSPA-C---YEDMGNNTANWRMLLRILPQSFGFIVPLLIMLFCYGFTLRTLFKAHMGQ
                                         ERLNATHCQYNFPQVG-----RTALRVLQLVAGFLLPLLVMAYCYAHILAVLLVSRGQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FLGLAHCCLNPMLYTFAGVKFRSDLSRLLTKLGCTGPASLCQLFPSWRR-SSLSESENAT
                                                                                                                                                                                    RSVTDVYLLNLALADLLFALTLPIWAASKVNGWIFGTFLCKVVSLLKEVNFYSGILLLAC
                                                                                                                                                                                                                                                                              SNYSYSSTLPPFLLDAAPCEPE-SLEINKYFVVIIYALVFLLSLLGNSLVMLVILYSRVG
                                                                                                                                   ISFDRYLNIVHATQLYRRGPPARVTLT------CLAVWGLCLLFALPDFIFLSAHHD
                                                                                                                                                                                                                                                                                                                                                                             141;
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                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                           51;
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EMBL:U11877; NID:g511818; PID:g511819; EMBL:U11878; NII
tens, L.L.; Bonner, T.I.; Kelvin, D.J.
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C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992
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A;Accession: S56162
A;Status: preliminary; nucleic acid sequence not shown
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Biochem. J. 309,
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C; Date: 27-Oct-1995 #sequence
C; Accession: S56162
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A; Residues: 1-327 <BAR>
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Pred. No. 4.8e-48;
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A; Molecule type: DNA
A; Residues: 1-355 <BEC>
A; Cross-references: GB:M74240; NID:g165438; PIDN:AAA33
A; Cross-references: GB:M74240; NID:g165438; PIDN:AAA33
R; Lee, J.; Kuang, W.J.; Rice, G.C.; Wood, W.I.
Immunol. 148, 1261-1264, 1992
A; Title: Characterization of complementary DNA clones
A; Reference number: A46483; MUID:92148149

PIDN: AAA31375.1;

PID:g165439

V.; Lyman,

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rabbit

B-TI

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interleukin-8 receptor (clone 5Bla) - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C;Accession: A53752
C;Pardo, G.N.; Thomas, K.M.; Suzuki, H.; LaRosa, G.J.; Wilkinson, N.; Folco, E.; Nava J. Biol. Chem. 269, 12391-12394, 1994
A.Title: Molecular characterization of a novel rabbit interleukin-8 receptor isotype. A;Reference number: A53752; MUID:94230294
A;Accession: A53752; MUID:94230294
A;Accession: A53752; MUID:94230294
A;Rolecular type: mRNA
A;Receptor isotype. MRNA
A;Residues: 1-358 < PRA>
A;Residues: 1-358 < PRA>
                                                                                                                                                                                                                                                                                                                       A;Cross-references: GB:L24445; NID:g437661; PIDN:AAA31378.1; PID:g437662 C;Superfamily: vertebrate rhodopsin C;Keywords: G protein-coupled receptor; transmembrane protein
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A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-355 <LEE>
A; Cross-references: GB:M82873; NID:g165440; PIDN:AAA31376.1; PID:g165441
A; Cross-references: neutrophils
A; Experimental source: neutrophils
A; Note: sequence extracted from NCBI backbone (NCBIN:81526, NCBIP:81530)
C; Superfamily: vertebrate rhodopsin
C; Keywords: G protein-coupled receptor; transmembrane protein
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Best Local
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Best Local
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                                                                                                                                                                                                                                                                    Local Similarity
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VNFYSGILLLACISVDRYLAIVHATRTMIQKR----HLVKFICLSMWGVSLILSLPILLFR
                                       INFYAGALLLACISFDRYLNIVHATQ--LYRRGPPARVTLTCLAVWGLCLLFALPDFIFL 237
                                                                                                                     AVAAVLLSRRTALSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGLCKVAGALFN 179
                                                                                                                                                                                                     ENFS-----SSYDYGENESDSCCTSPPCPQDFSLNFDRAFLPALYSLLFLLGLLGNG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YAGALLLACISFDRYLNIVHATQLYRRGPPARVTLT------CLAVWGLCLLFALPD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NFSSSYDYGENESDSCCTSPPCPQDFS-----LNFDRAFLPALYSLLFLLGLLGNGAVA 122
                                                                               LVMLVILYSRSTCSVTDVYLLNLAIADLLFATTLPIWAASKVHGWTFGTPLCKVVSLVKE
                                                                                                                                                               ENYSYEDFFGDFSNYSYSTDLPPTLLDSAPCRSE-SLETNSYVVLITYILVFLLSLLGNS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AVILSRRTALSSTDTFILHLAVADTLLVLTLPLWAVDAAVQWVFGSGLCKVAGALFNINF 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NMTDLWTWFEDEFANATGMPPVEKDYSPCLVVTQTLNKYVVVVIYALVFLLSLLGNSLVM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           136;
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                                                                                                                                                                                                                                                                28.6%;
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                                                                                                                                                                                                                                                                Score 615; DB 2;
Pred. No. 1.5e-46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 615.5;
Pred. No. 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches 130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .4e-46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2;
                                                                                                                                                                                                                                                                                   Length 358;
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A;Cross-references: EMBL:X65858; NID:g312046; PIDN:CAA46688.1; R;Ahuja, S.K.; Shetty, A.; Tiffany, H.L.; Murphy, P.M.
J. Biol. Chem. 269, 26381-26389, 1994
A;Title: Comparison of the genomic organization and promoter full approximation of the genomic organization and promoter full a; Reference number: 137898; MUID:95014476
A; Accession: 138710
A; Molecule type: DNA
A; Residues: 1-350 <RE2>
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A;Title: Structure and functional expression of a human interle A;Reference number: A39445; MUID:91368199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Homo sapiens (man)
C;Date: 22-Jan-1993 #sequence_revision 12-Apr-1996 #text_change 05-Nov-1999
C;Accession: 137449; 118710; I38711; A39445
R;Mollereau, C:; Muscatelli, F:; Mattei, M.G.; Vassart, G.; Parmentier, M. Genomics 16, 248-251, 1993
A;Title: The high-affinity interleukin 8 receptor gene (IL8RA) maps to the A;Reference number: 137449; MUID:93252387
A;Accession: 137449
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C; Superfamily: vertebrate
C; Keywords: G protein-coup
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A;Molecule type: mrNA
A;Residues: 1-275,'T','277-350 <HOL>
A;Cross-references: GB:M68932; NID:g186369; PIDN:AAA59159.1; PID:g186370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-16 < RE3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-350 < RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N;Alternate names: interleukin-8 receptor,
C;Species: Homo sapiens (man)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GDB:135039; OMIM:146929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Gene: GDB:IL8RA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A39445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 interleukin-8 receptor type A - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Superfamily: vertebrate rhodopsin Keywords: G protein-coupled receptor; glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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                           253
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                                                                                                                       HATQLYRRGPPARVTLT--
                                                                                                                                                                                                                                                                                                                     PPCPQDFS-----LNFDRAFLPALYSLLFLLGLLGNGAVAAVLLSRRTALSSTDTFLLH 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GFLHSCLNPITYAFIGQKFRYGLLKILAAHGLISKEFLAKESRPSFVASSSGNTS 355
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                                                                                                                                                                    LALADLLFALTLPIWAASKVNGWIFGTFLCKVVSLLKEVNFYSGILLLACISVDRYLAIV
                                                                                                                                                                                                                  LAVADTLLVLTLPLWAVDAAVQWVFGSGLCKVAGALFNINFYAGALLLACISFDRYLNIV 201
                                                                                                                                                                                                                                                                  PPADEDYSPCMLETETLNKYVVIIAYALVFLLSLLGNSLVMLVILYSRVGRSVTDVYLLN 80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SAHHDERLNATHCQY----NFPQVGRTALRVLQLVAGFLLPLLVMAYCYAHILAVLLVSR
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                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                    NFPQVGRTALRVLQLVAGFLLPLLVMAYCYAHILAVLLVSRGQRRLRAMRLVVVVV
                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                    -----TLTQKRHLVKFVCLGCWGLSMNLSLPFFLFRQAYHPN--NSSPVCY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL:U11870; NID:g511804; PIDN:AAA64378.1;
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                                                                                                                                                                                                                                                                                                                                                                                         28.2%; Score 606.5; DB 2 39.7%; Pred. No. 8.4e-46;
50;
                                                                                                                  -- CLAVWGLCLLFALPDFIFLSAHHDERLNATHCQY
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R;Schweickart, V.L.; Raport, C.J.; Godiska, R.; Byers, M.G.; Eddy Jr., R.L.; She Genomics 23, 643-650, 1994
A;Title: Cloning of human and mouse EBI1, a lymphoid-specific G-protein-coupled A;Reference number: A55735; MUID:95154835
A;Accession: B55735
                                                                                                                                                         lymphocyte-specific G protein-coupled N; Alternate names: Burkitt's lymphoma C; Species: Homo sapiens (man) C; Date: 07-Jul-1995 #sequence_revision C; Accession: B55735; S52443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: EMBL:X77797
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 10
S42096
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-378 <SCI
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B55735
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A; Residues: 1-356 <GOB>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Interleukin-8 receptor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 06-Jan-1995 #sequence_revision 06
C;Accession: S42096
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                                                                                                                 ;Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 19-May-2000;Accession: B5573; S52443;Accession: B5573; S52443
;Accession: B5573; S52443
enomics 23, 643-650, 1994
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Best Local
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                                                                                                                                                                                                                                                                                                                                          FLHSCLNPIIYAFIGQKFRHGLLKIMANYGLVSKEFLAKEGRPSFVGSSSANTS
                                                                                                                                                                                                                                                                                                                                                                                YMHCCLNPLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSSWSETS
                                                                                                                                                                                                                                                                                                                                                                                                                                                   VKANPSTVVCYEN---IGNNTSKWRVVLRILPQTYGFLLPLLIMLFCYGFTLRTLFKAHM 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LVILYNRSTCSVTDVYLLNLAIADLFFALTLPVWAASKVNGWIFGSFLCKVFSFLQEITF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AVLLSRRTALSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGLCKVAGALFNINF 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENFSS----SYDYGENESDSCCTSPPCPQDFSLNFDRAFLPALYSLLFLLGLLGNGAVA 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GQNFRHGFLKILAMHGLVSKEFLARHRVTSYTSSSVNVSS 348
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                                                                                                                                                                                                                                                                                                                                                                                                                          GQKHRAMRVIFAVVLVFLLCWLPYNIVLFTDTLMRTKLIKETCERQNEINKASEI---LG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YSSVLLLACISMDRYLAIVHATSTLIQKR----HLVKFVCITMWFLSLVLSLPIFI-LRTT 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YAGALLLACISFDRYLNIVHATQ -- LYRRGPPARVTLTCLAVWGLCLLFALPDFIFLSAH 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSSWSETS 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVTSGLGYMHCCLNPLLYAFV 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HDERLNATHCQYNFPQVG-----RTALRVLQLVAGFLLPLLVMAYCYAHILAVLLVSRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LEDFFSGDIDSYNFSSDPPFTLSDAAPCP-SANLDINRYAVVVIYVLVTLLSLVGNSLVM 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EVLGNDTAKWRMVLRILPHTFGFIVPLFVMLFCYGFTLRTLFKAHMGQKHRAMRVIFAVV
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38.1%;
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Pred. No. 1.2e-44;
50; Mismatches 136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    February 1994
                                                                                                                                                                                                                    receptor
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                                                                                                                                                                                                                  EBIl - human
2; Epstein-Barr virus induced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2;
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                                                                                                                                      Shows,
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fusin (LESTRA) - crab-eating macaque
c;Species: Macaca fascicularis (crab-eating macaque)
C;Date: 11-Apr-1997 #sequence_revision 11-Apr-1997 #
C;Accession: G00048
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Description: The expression of the chemokine receptor A;Reference number: $52443 A;Accession: $52443
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                                                                                                                                                                                      A;Cross-references: GB:D86579; NID:g1468948; PID:g1468949 C;Superfamily: vertebrate rhodopsin
                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 1-352 <TAT>
                                                                                                                                                                                                                                                              A; Status: preliminary; translated from GB/EMBL/DDB
                                                                                                                                                                                                                                                                                 A; Reference number: A; Accession: G00048
                                                                                                                                                                                                                                                                                                                        submitted to GenBank,
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A; Cross-references: EMBL: X84702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GB:L31581; NID:g468319; PIDN:AAA74231.1; R;Burgstahler, R.; Kempkes, B.; Staeube, K.; Lipp, M. submitted to the EMBL Data Library, February 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local S
Matches 133
                                                                                                                Matches
                                                                                                                                                     Query Match
   128
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les 133; Conserv
                                                                                                                                    Local
RRTALSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGLCKVAGALFNINFYAGAL 187
                                                      VGVKFRERMWMLLLRLGCPNQRGLQRQPSSSR--RDSSWSETSEAS 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TMTDTYLLNLAVADILFLLTLPFWAYSAAKSWVFGVHFCKLIFAIYKMSFFSGMLLLLCI 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGLCKVAGALFNINFYAGALLLACI 192
                                      DNYTEEMGSGDYDS----IKEPCFREENAHFNRIFLPTIYSIIFLTGIVGNGLVILVMGY 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IGVKFRNDLFKLFKDLGCLSQEQL-RQWSSCRHIRRSSMSVEAETT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEDRYLNIVHATQLYRRGPPARV----TLTCLAVWGLCLLFALPDFIFLSAHHDERLNAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DYIGDNTTVDYTLFESLCSKKDVRNFKAWFLPIMYSIICFVGLLGNGLVVLTYIYFKRLK 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DY-GENES-DSCCTSPPCPQDFSLNFDRAFLPALYSLLFLLGLLGNGAVAAVLLSRRTAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VVVFIVFQLPYNGVVLAQTVANFNITSSTCELSKQLNIAYDVTYSLACVRCCVNPFLYAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HCQYNFPQV-GRTALRVLQLVAGFLLPLLVMAYCYAHILAVLLVSRGQRRLRAMRLVVVV
                                                                                                                  123;
                                                                                                                                    Similarity
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                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                     H00048
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                                                                                                                                  27.1%;
35.4%;
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                                                                                                                70;
                                                                                                                                  Score 582.5; DB 2; Pred. No. 1.1e-43;
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                                                                                                                Mismatches
                                                                                                              1.1e-43;
ches 137;
                                                                                                                                                                                                                                                                                                                                                                           #text_change
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                                                                                                                                                   Length 352;
                                                                                                                Indels
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                                                                                                                17;
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Вþ

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QKKLRSMTDKYRLHLSVADLLYVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNLYSSVL

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C:Species: Homo sapiens (man)
C:Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 05-Nov-1999
C:Accession: A45747; A53103; I53006; I59444; I69203; S33761
R:Federsppiel, B.; Melhado, I.G.; Duncan, A.M.V.; Delaney, A.; Schappert, K Genomics 16, 707-712, 1993
                                                                                                                                                                                                                                                                          Int. Immunol. 5, 1239-1249, 1337
A;Title: Molecular cloning of cDNAs encoding a LD78 receptor
A:Reference number: I54751; MUID:94092629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Title: A proposed bovine neuropeptide Y A;Reference number: I59444; MUID:94052833 A;Accession: I59444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GB:L06797; NID:g414929; PIDN:AAA03209.1; PID:g414928 R;Jazin, E.E.; Yoo, H.; Blomqvist, A.G.; Yee, F.; Weng, G.; Walker, M.W. Regul. Pept. 47, 247-258, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: EMBL:X71635; NID:g297099; PIDN:CAA50641.1; R;Herzog, H.; Hort, Y.J.; Shine, J.; Selbie, L.A. DNA Cell Biol. 12, 465-471, 1993
A;Title: Molecular cloning, characterization, and localization A;Reference number: I53006; MUID:93319629
A;Accession: I53006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GB:M99293; NID:g292516; PIDN:AAA16617.1; PID:g292517 R;Loetscher, M.; Geiser, T.; O'Reilly, T.; Zwahlen, R.; Baggiolini, M.; J. Biol. Chem. 269, 232-237, 1994
A;Title: Cloning of a human seven-transmembrane domain receptor, LESTR, A;Reference number: A53103; MUID:94103215
A;Accession: A53103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Title: Molecular cloning of the cDNA and A; Reference number: A45747; MUID:93315164 A; Accession: A45747
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A; Map position:
C; Superfamily: v
                                                       A; Cross-references:
                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 1-352 < RES>
                                                                                                                                                                                                                                                             A; Reference number: I54751;
A; Accession: I69203
                                                                                                                                                                                                                                                                                                                                                   R; Nomura, H.; Nielsen, B.W.; Matsushima, K. Int. Immunol. 5, 1239-1249, 1993
                                                                                                                                                                                                                                                                                                                                                                                                             A;Residues: 1-352 <RE2>
A;Cross-references: GB:L01639; NID:g189313; PIDN:AAA16594.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-352 <LOE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-352 <FED>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            neuropeptide Y/peptide YY receptor Y3 - human
N;Alternate names: fusin; HM89; leukocyte-derived seven-transmembrane receptor LESTR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             밁
                                                                                                                 C; Genetics:
                                                                                                                                               A; Cross-references:
                                                                                                                                                                                                                                  A; Status: preliminary; translated from GB/EMBL/DDBJ
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A; Residues: 1-352 <HER>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             247
                                                                                  GDB:NPY3R; NPYY3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AFVGVKFRERMWMLL------LRLGCPNQRGLQRQPSSSRRDSSW 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATHCQYNFP-QVGRTALRVLQLVAGFLLPLLVMAYCYAHILAVLLVSRGQRRLRAMRLVV 305
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --ICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKTTV
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                              2q21-2q21
                                                       GDB:230002; OMIM:162643
                                                                                                                                         GB:D10924; NID:g219868; PIDN:BAA01722.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (NPY) receptor cDNA clone, or its human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    chromosomal localization of the gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Delaney, A.; Schappert, K.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Walker, M.W.; Salon,
                                                                                                                                                                                                                                                                                                                                                                                                             PID:g189314
                                                                                                                                            PID:g219869
                                                                                                                                                                                                                                                                                                                       and putative leukocyte chem
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C;Species: Mus musculus (house mouse)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 05-Nov-1999
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 05-Nov-1999
C;Accession: A48921; A53677; I49348; I55421; H48909; I53774
R;Cerretti, D.P.; Nelson, N.; Kozlosky, C.J.; Morrissey, P.J.; Copeland, N.G.; Gilber Genomics 18, 410-413, 1993
A;Title: The murine homologue of the human interleukin-8 receptor type B maps near th A; Reference number: A48921; MUID:94117014
A;Accession: A48921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross references: GB:L23637; NID:g435093; R;Suzuki, H.: Prado, G.N.: Wilkinson, N.; NaJ. Biol. Chem. 269, 18263-18266; 1994
A;Title: The N terminus of interleukin-8 (II A;Reference number: A53677; MUID:94308043
A;Accession: A53677
                                                                                                                                                                                                                                                                                          A; Title: Chemokine binding and activities A; Reference number: I49348; MUID:95363183 A; Accession: I49348
                                                                                                                                                                                                                                                                                                                                                           A; Note: sequence extracted from NCBI backbone (NCBIP:149812) R; Lee, J.; Cacalano, G.; Camerato, T.; Toy, K.; Moore, M.W.; J. Immunol. 155, 2158-2164, 1995
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                           A; Molecule
                                          A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                     A;Reference number: I55421; MUID:95050766
A;Accession: I55421
                                                                                                                  R;Bozic, C.R.; Gerard, N.P.; von Uexkull-Guldenband, C.; Kol
J. Biol. Chem. 269, 29355-29358, 1994
A;Title: The murine interleukin 8 type B receptor homologue
                                                                                                                                                                    A;Cross-references: EMBL:U31207; NID:g950174; PIDN:AAC52239.1; PID:g950175 R;Bozic, C.R.; Gerard, N.P.; von Uexkull-Guldenband, C.; Kolakowski, L.F.
                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-359 < RES>
                                                                                                                                                                                                                                                                   A; Status: preliminary; translated from GB/EMBL/DDB:
                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Cross-references: GB:L26549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Residues: 1-359 <SUZ>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: nucleic acid sequence not A;Molecule type: DNA
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A; Residues: 1-359 < CER>
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N; Alternate names: G-protein coupled receptor Gpcr16
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type: DNA: 1-359 <RE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RRTALSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGLCKVAGALFNINFYAGAL 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNYTEEMGSGDYDS----MKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVILVMGY 65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNLYSSVL 125
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    <RE2>
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35.0%;
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Pred. No. 3.8
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Copeland,

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neuropeptide Y/peptide YY receptor Y3 - bovine C;Species: Bos primigenius taurus (cattle) C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_chang C;Accession: S28787
C;Accession: S28787
MO1. Pharmacol. 40, 869-875, 1991
A;Title: Sequence and expression of a neuropeptide Y receptor A;Reference number: S28787; MUID:92100053
A;Accession: S28787
A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                          RESULT 15
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A;Cross-references: GB:L20337; NID:g438800; PIDN:AAA16853.1; PID:g438801
A;Cross-references: GB:L20337; NID:g438800; PIDN:AAA16853.1; PID:g438801
A;Harada, A.; Kuno, K.; Nomura, H.; Mukaida, N.; Murakami, S.; Matsushima, K.
Gene 142, 297-300, 1994
A;Title: Cloning of a cDNA encoding a mouse homolog of the interleukin-8 receptor.
A;Reference number: I53774; MUID:94252584
A;Accession: I53774
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A;Molecule type: mRNA
A;Residues: 1-359 <RE3>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HDERLNATHCQYNFPQVG-----RTALRVLQLVAGFLLPLLVMAYCYAHILAVLLVSRG 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YSSVLLLACISMDRYLAIVHATSTLIQKR---HLVKFVCIAMWLLSVILALP-ILILRNP 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YAGALLLACISFDRYLNIVHATQ--LYRRGPPARVTLTCLAVWGLCLLFALPDFIFLSAH 240
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                                                                                                                                                                                                    17-Apr-1993 #text_change 26-Aug-1999
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A;Cross-references: EMBL:M86739
C;Superfamily: vertebrate rhodopsin
C;Keywords: appetite; G protein-coupled receptor; transmembrane protein
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AFLGAKFKTSAOHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSF
                                                                                                                                          ILAFISLDRYLAIVHATNSQKPRKLLAEKVVYVGVWLPAVLLTIPDLIFADIKEVDERY- 185
                                                                                                                                                                                                         RRTALSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGLCKVAGALENINFYAGAL 187
                                                                                                                                                                                                                                                                                                                              ENFSSSYDYGENESDSCCTSPPCPQDFSLNFDRAFLPALYSLLFLLGLLGNGAVAAVLLS 127
                              AFVGVKFRERMWMLL-----LRLGCPNQRGLQRQPSSSRRDSSW
                                                                                        VVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVTSGLGYMHCCLNPLLY 365
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CCR4_FELCA
ILBB_MOUSE
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Best Local S
Matches 364
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EMBL; Z79783;
EMBL; U32674;
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DISULFID
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
TRANSMEM
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DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR004070; CXCchemok_receptor3.
InterPro; IPR000276; GPCK_Rhodpsn.
Pfam; PF00001; 7tm.1; 1.
PRINTS; PR001532; CXCCHMKINER3.
PRINTS; PR00337; GPCRRHODOPSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCRDb; GCR_1341; -. GCRDb; GCR_1972; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 600894; -
SYSGL 368
                                    SYSGL 415
                                                                                           SGLGYMHCCLNPLLYAFYGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSSWSETSEA
                                                                                                                                                                   VSRGQRRLRAMRLVVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVT
                                                                                                                                                                                                                         LPDFIFLSAHHDERLNATHCQYNFPQVGRTALRVLQLVAGFLLPLLVMAYCYAHILAVLL
                                                                                                                                                                                                                                         LPDFIFLSAHHDERLNATHCQYNFPQVGRTALRVLQLVAGFLLPLLVMAYCYAHILAVLL
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                                                                       SGLGYMHCCLNPLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSSWSETSEA
                                                                                                                                               VSRGQRRLRAMRLVVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVT
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CAB02143.1;
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99.7%;
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CYTOPLASMIC (PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 1891; DB 1; Pred. No. 1.7e-123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
A -> R (IN REF. 2).
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5 (POTENTIAL)
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3 (POTENTIAL)
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2 (POTENTIAL)
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BY SIMILARITY.
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7 (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F08A3B44B2BBAD04 CRC64;
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RESULT 2

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DT 16-OCT
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DT 16-OCT
DT 16-OCT
CCC CC MAMMAL
OC EMAMAL
OC MAMMAL
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RA Jenkin
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PRINTS; PRO1532; CXCCHMKINER3.

PRINTS; PRO0237; GPCRRHODOPSN.

PROSITE; PS00237; G_PROTEIN_RECEP_F1_2; 1.

PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.

G-protein coupled receptor; Transmembrane;

DOMAIN

52
TRANSMEM
53
79
1 (POTENTIAL)

DOMAIN
80
88
CYTOPLASMIC
7 (POTENTIAL)
7 (POTENTIAL)
                                                                                                                                                                                                                     DOMAIN
DISULFID
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCR3_MOUSE
O88410;
                                                                                                                                                                                                                                                                                                                                                       TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commensentities requires a license agreement (See http://www.isb-sib.ch/annot or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "The CC chemokine 6Ckine binds the CXC chemokine receptor CXCR3.";
Proc. Natl. Acad. Sci. U.S.A. 95:8205-8210(1998).
-i- FUNCTION: RECEPTOR FOR SCYB9/MIG, SCYB10/INP10 AND SCYB11/ITAC SIMILARITY). BINDS TO SCYA21.
-i- SUBCELLULAR LOCATION: Integral membrane protein.
-i- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
C-X-C chemokine receptor type 3 (CXC-R3) (CXCR-3).
                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                              CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 between the Swiss Institute of Bioinfo
the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Soto H., Wang W., Strieter R.M., Cop
Jenkins N.A., Hedrick J., Zlotnik A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CXCR3 OR CMKAR3
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                                            51
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                      SWISS-PROT entry is copyright. It is produced through a ceen the Swiss Institute of Bioinformatics and the EMBL
EVSERQVLDASDFAFILENSTSPYDYGENESD-FSDSPPCPQDFSLNFDRTFLPALYSLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PF00001;
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                                                                                                           Similarity
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IPR000276; GPCR_Rhodpsn.
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                                                                                       Conservative
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                                                                                                         75.6%;
                                                                                                                                                                            MW.
                                                                                Score 1626.5;
Pred. No. 2.8e
22; Mismatches
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                                                                                                                                                                        7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
BY SIMILARITY.
N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL);
029FBB778E3CD4EA CRC64;
                                                                                                                                                                                                                                                                                   EXTRACELLULAR (POTENTIAL)
7 (POTENTIAL)
                                                                                                                                                                                                                                                                                                                              CYTOPLASMIC 6 (POTENTIAL)
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4 (POTENTIAL
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2 (POTENTIA)
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934997;
01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
C-X-C chemokine receptor type 5 (CXC-R5) (CXCR-5) (Burkitt'S lymphoma receptor 1 homolog) (Neurolymphatic receptor) (NLR).
                                                                                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entitles requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=93238948; PubMed=8386678; Kouba M., Vanetti M., Wang X., Schaefer M., Hoellt V.; Kouba M., Vanetti M., Wang X., Schaefer M., Hoellt V.; "Cloning of a novel putative G-protein-coupled receptor (NI is expressed in neuronal and lymphatic tissue."; FEBS Lett. 321:173-178(1993).

-i- FUNCTION: CYTOKINE RECEPTOR THAT BINDS TO B LYMPHOCYTE
                                                                                                                                                                                                                                                                                                                        EMBL; X71463; CAA50582.1; PIR; S32785; S32785.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BLR1 OR CXCR5
      TRANSMEM
                                                            TRANSMEM
                                                                                           DOMAIN
                                                                                                                      G-protein
                                                                                                                                                                                                                                                                  InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               between
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus (Rat).
                                                                                                                                                                                                                                         Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way lifted and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHEMOATTRACTANT (BLC) (BY SIMILARITY).
SUBCELLULAR LOCATION: Integral membrane protein.
TISSUE SPECIFICITY: EXPRESSED IN NEURONAL AND LYMPHATIC TISSUE.
SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SYLGL 367
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Pro; IPR000276; GPCR_Rhodpsn.
PF00001; 7tm_1; 1.
S; PR00237; GPCRRHODDPSN.
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E; PS00237; G_PROTEIN_RECEP_F1_1; 1.
E; PS50262; G_PROTEIN_RECEP_F1_2; 1.
ein coupled receptor; Transmembrane; Gl
57 EXTRACELLULAR (P
1 57 EXTRACELLULAR (P
1 79 90 CYTOPLASNIC (POT
EM 91 111 2 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rat
                              (POTENTIAL)
                                                                                                                Glycoprotein;
                                                                                     (POTENTIAL).
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CCR5_MOUSE
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SEQUENCE FROM N.A.
STRAIN-BALB/C; TISSUE-Liver;
K MEDLINE-94009211; PubMed-8405054;
K Maiser E., Foerster R., Wolf I., Epensperger C., Kue The G protein-coupled receptor BLR1 is involved in differentiation and is also expressed in neuronal to the following strain of the following strains of the follow
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Best Local S
Matches 146
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01-OCT-1993
30-MAY-2000
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TRANSMEM
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30-MAY-2000 (Rel. 39, Last annotation update)
C-X-C chemokine receptor type 5 (CXC-R5) (CXCR-5) (Burkitt'S lymphoma
MEDLINE-94116980;
Wilkie T.M., Chen
Copeland N.G., Je
                                                                                                                                                                                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10090;
                                                        TISSUE-Testis;
                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                               receptor 1 homolog).
BLR1 OR CXCR5 OR GPCR6.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Q04683;
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                 Chen
   Jenkins
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                  Y., Gilbert D.J
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Rodentia;
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N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
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                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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                  K.J.,
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l tissues.";
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; Murinae; Mus
                    Simon
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                                                                                                                                               Lipp
cell
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                                                                                     Query Match
Best Local
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                                                                                   DISULFID SEQUENCE
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DOMAIN
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DOMAIN
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                           CARBOHYD
                                                                                                                                    DOMAIN
                                                                                                                                                TRANSMEM
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                                                                                                                                                                                                                                               TRANSMEM
                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                          PRINTS;
                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00001;
                                                                                                                                                                                                                                                                                                                                                                                          GCRDb; GCR_0832; -. MGD; MGI:103567; Blr1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Burkitt's lymphoma receptor-1."; Nature 391:799-803(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=98146056;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      defined lymphoid organs and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=97133211; PubMed=8978608; Foerster R., Mattis A.E., Kremmer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Identification, chromosomal location, and genome organization mammalian G-protein-coupled receptors."; Genomics 18:175-184(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mammalian
                                                                                                                                                                        TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000276; GPCR_Rhodpsn
Pfam; PF00001; 7tm_1; 1.
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             70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  erster R., Mattis A.E., Kremmer E.,
putative chemokine receptor, BLR1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        B-cell-homing chemokine made
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FOLLICLES OF SPLEEN AND PEYER'S PATCHES, BUT NOT IN THOSE OF MESENTRIC OR PERIPHERAL LYMPH NODES.
SUBCELLULAR LOCATION: Integral membrane protein.
TISSUE SPECIFICITY: MAINLY IN SPLEEN, IN RESTING B-CELLS.
SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 European Bioinformatics Institute. The by non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: CYTOKINE RECEPTOR THAT BINDS TO CHEMOATTRACTANT (BLC). INVOLVED IN B-CELL
FSSSYDYGENESDSCCTSPPCPQDFSLNFDRAFLPALYSLLFLLGLLGNGAVAAVLLSRR 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              M.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               87:1037-1047(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                        PR00237; GPCRRHODOPSN
                                                 Similarity
                                                                                                                                                                                                                                                                                                                                  PS00237;
PS50262;
                                                                                                                                                                                                                                                                                                                     coupled
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243
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283
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198
                                    Conservative
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                                                                                                                                                                                                                                                                                                                                 G_PROTEIN_RECEP_F1_1; 1.
G_PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                                                                                                                                                         receptor;
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                                                                                     42100
                                                29.8%;
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                                                                                     MW.
                                   54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    remmer E., Wolf E., Brem G., Lipp M.;
tor, BLR1, directs B cell migration to
specific anatomic compartments of the
                                                                                                                                                                                                                                                                                                                   RECEP_F1_2; 1.
Transmembrane;
                                   Pred. No. 2.4e
; Mismatches
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                                                                                                                                  7 (POTENTIAL)
CYTOPLASMIC (
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4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
5 (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
3 (POTENTIAL).
                                                Score 640;
Pred. No. 2.
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6 (POTENTIAL
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7 (POTENTIAL).
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                                              DB 1;
.4e-37;
                                                                                                                                  (POTENTIAL)
                                                                                                                                                                                 (POTENTIAL).
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L MIGRATION INTO B-
BUT NOT IN THOSE (
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                                   Indels
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                                    14;
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01-OCT-1993 (Rel. 2
01-OCT-1993 (Rel. 2
16-OCT-2001 (Rel. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Sequence variation of a novel heptahelical leucocyte receptor through alternative transcript formation.";

piochem. J. 309:773-779(1995).
                                                                                                                                                                                                                                                                                                                                                                     Legler D.F., Lo
Baggiolini M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Blood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Differentiation-specific expression receptor from Burkitt's lymphoma."; cur. J. Immunol. 22:2795-2799(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-93049615; PubMed=1425907;
Dobner T., Wolf I., Emrich T., Lipp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human)
Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C-X-C chemokine receptor type receptor 1) (Monocyte-derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCR5_HUMAN
                                                                                                                                                                                                                                                                    J. Exp. Med. 187:655-660(1998)
                                                                                                                                                                                                                                                                                                BLR1/CXCR5
                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=98130629;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  LIGAND BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE~95366951;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. (SHORT FORM).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                            "B cell-attracting chemokine 1,
                                                                                                                                                                                                                                                                                                                     Lymphoid tissues,
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                                           POSSIBLY A REGULATORY FUNCTION IN BURKITT LYMPHOM LYMPHOMAGENESIS AND/OR B-CELL DIFFERENTIATION. IT CANDIDATE FOR CELL-CELL INTERACTION, AND ACTIVATI LYMPHOCYTES IN LYMPHATIC TISSUES.

SUBCELLULAR LOCATION: Integral membrane protein. ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SH SHORT FORM, ARE PRODUCED BY ALTERNATIVE SPLICING. TISSUE SPECIFICITY: EXPRESSION IN MATURE B-CELLS
                                                                                                                                                                                        ACXCKS. (ACXCKS. (ACXCKS).

SXP. Med. 187:655-660(1998).

FUNCTION: CYTOKINE RECEPTOR THAT BINDS TO BLC. BLRL BETT LYMPHOMA (BETTT)

FUNCTION: OF REGULATORY FUNCTION IN BURKITT LYMPHOMA (BETTT)

FOR THE PROPERTY OF THE PRO
                         LYMPHOMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OR CXCR5.
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                            CELLS
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BELONGS
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27, Last sequence update)
40, Last annotation update)
40, Last annotation update;
ceceptor type 5 (CXC-R5) (CXCR-5) (Burkitt'S lymphomanorederived receptor 15) (MDR15).
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FAMILY
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G-PROTEIN COUPLED
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PIR; S26667; S26667.
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PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.

G-protein coupled receptor: Transmembrane; Glycoprotein;

Alternative splicing; Polymorphism.
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PRINTS; PR00237; GPCRRHODOPSN.
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FIGLAHCCLNPMLYTFAGVKFRSDLSRLLTKLGCTGPASLCQLFPSWRR-SSLSESENAT
                       GLGYMHCCLNPLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSSWSETSEAS
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CYTOPLASMIC (POTENTIAL).
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"Cloning of complementary DNA encoding interleukin-8 receptor.";
Science 253:1280-1283(1991).
    the
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MEDLINE-9235587;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ahuja S.K., Shetty A., Tiffany H.L., Mury "Comparison of the genomic organization thuman interleukin-8 receptors A and B.", J. Biol. Chem. 269:26381-26389(1994).
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01-FEB-1996 (Rel. 33, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
High affinity interleukin-8 receptor B (IL-8R
                               between
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Molecular characterization of receptors for human interleukin-8, RO/melanoma growth-stimulatory activity and neutrophil activating
                                                                            BIOI. Chem. 267:16283-16287(1992).

FUNCTION: RECEPTOR TO INTERLEUKIN'8, WHICH IS A POWERFUL FUNCTION: RECEPTOR TO INTERLEUKIN'8, WHICH IS A POWERFUL NEUTROPHILS CHEMOTACTIC FACTOR. BINDING OF IL-8 TO THE RECEPTOR CAUSES ACTIVATION OF NEUTROPHILS. THIS RESPONSE IS MEDIATED VIA G-PROTEIN THAT ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM. THIS RECEPTOR BINDS TO IL-8 WITH A HIGH AFFINITY AND TO GRO/MGSA AND NAP-2 ALSO WITH A HIGH AFFINITY.

SUBCELLULAR LOCATION: Integral membrane protein.

SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DATABASE: NAME-PROW; NOTE-CD guide CDw128b entry;

WWW-"http://www.ncbi.nlm.nih.gov/prow/cd/cdw128b.htm".
       European
SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN European Bioinformatics Institute. There are no restream
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PIR; A53611; A53611.

HSSP; P34996; IDDD.

GCRDb; GCR_0077; --

GCRDb; GCR_0610; --
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PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCRDb; GCR_1339; -. GCRDb; GCR_1831; -. MIM; 146928; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000276; GPCR_Rhodpsn.
InterPro; IPR000832; GPCR_secretin.
Pfam; PF00001; 7tm_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 G-protein coupled
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                                                                                       246
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M94582; AAA36108.1;

M99412; AAC14460.1;

L19593; AAB59437.1;

U11869; AAB60656.1;
                                                 HSCLNPLIYAFIGQKFRHGLLKILAIHGLISKDSLPKDSRPSFVGSSSGHTS
                                                          HCCLNPLLYAFYGYKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSSWSETS
                                                                                      SNVSPA-C---YEDMGNNTANWRMLLRILPQSFGFIVPLLIMLFCYGFTLRTLFKAHMGQ
                                                                                                                                                                              RSVTDVYLLNLALADLLFALTLPIWAASKVNGWIFGTFLCKVVSLLKEVNFYSGILLLAC
                                                                                                                                                                                                                             LSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGLCKVAGALFNINFYAGALLLAC 191
                                                                                                                                                                                                                                                SNYSYSSTLPPFLLDAAPCEPE-SLEINKYFVVIIYALVFLLSLLGNSLVMLVILYSRVG 79
                                                                                                                                                                                                                                                                   SSYDYGENESDSCCTSPPCPQDFSLNFDRAFLPALYSLLFLLGLLGNGAVAAVLLSRRTA 131
                                                                                                        RLRAMRLVVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVTSGLGYM
                                                                                                                                                 ERLNATHCQYNFPQVG---
                                                                                                                                                                     ISVDRYLAIVHATR---
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                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                               360
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49
76
85
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143
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 STANDARD;
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40.1%;
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                                                                                                                                                                                                                                                                                                                              MW;
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                                                                                                                                                                                                                                                                                        51;
                                                                                                                                                 RTALRVLQLVAGFLLPLLVMAYCYAHILAVLLVSRGQR
                                                                                                                                                                                                                                                                                                                                                       EXTRACELLULAR (POTENTIAL).
5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                             EXTRACELLULAR (POTENTIAL).

1 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
3 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Transmembrane; Glycoprotein.
                                                                                                                                                                                                                                                                                                Score 633; DB 1;
Pred. No. 7.1e-37;
                                                                                                                                                                                                                                                                                                                            N-LINKED (GLCNAC. . .) (POTENTIAL).
BY SIMILARITY.
564F04A8BCCOA197 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                    3 (POTENTIAL)
CYTOPLASMIC (1
 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                             (POTENTIAL)
                                                                                                                                                                                                                                                                                        Mismatches
 353
 B
                                                                                                                                                                                                                                                                                                                                                                                                                                     (POTENTIAL)
                                                                                                                                                                                                                                                                                        130;
                                                                                                                                                                                                                                                                                                        Length 360;
                                                                   408
                                                 357
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Best Local S
Matches 143
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01-NOV-1997 (Rel. 3
01-NOV-1997 (Rel. 3
High affinity inter
                                                                                                                                                              NON_TER
SEQUENCE
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TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      modified and this statement is not removentities requires a license agreement (Sor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    G-protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Macaca mulatta (Rhesus macaque)
                                                                                                                                                                                                       CARBOHYD
                                                                                                                                                                                                                               DISULFID
                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                      TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chemotaxis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS50262;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00237;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000276; GPCR_Rhodpsn.
InterPro; IPR000832; GPCR_secretir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X91116; CAA62565.1;

    -!- SUBCELLULAR LOCATION: Integral membrane protein.
    -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Characterization of interleukin-8 receptors in non-human primates.";
Immunogenetics 43:261-267(1996).
-i- FUNCTION; RECEPTOR TO INTERLEUKIN-8, WHICH IS A POWERFUL-
NEUTROPHILS CHEMOTACTIC FACTOR. BINDING OF IL-8 TO THE RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alvarez V., Coto
Lopez-Larrea C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. MEDLINE=96175151;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cercopithecinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IL8RB OR CXCR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q28519;
                                                                                                                                                                                                                                                                                                            TRANSMEM
15
                                        89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            G-PROTEIN THAT ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM. THIS RECEPTOR BINDS TO IL-8 WITH A HIGH AFFINITY AND TO GRO/MGSA AND NAP-2 ALSO WITH A HIGH AFFINITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NEUTROPHILS CHEMOTACTIC FACTOR. BINDING OF IL-8 TO THE RECEPTOR CAUSES ACTIVATION OF NEUTROPHILS. THIS RESPONSE IS MEDIATED VIA A
                       ENFSSSYDYGENESDSCCTSPPCPQDFSLNFDRAFLPALYSLLFLLGLLGNGAVAAVLLS
EDF-SNYSYSSDLPPSLPDVAPCRPE-SLEINKYFVVIIYALVFLLSLLGNSLVMLVILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P34996; 1DDD
                                                                                                  Similarity
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                                                                                                                                                              353
                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7tm_1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 G_PROTEIN_RECEP_F1_1; 1.
G_PROTEIN_RECEP_F1_2; 1.
receptor; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35, Created)
35, Last sequence update)
35, Last annotation update)
erleukin-8 receptor B (IL-8R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PubMed=9110929;
                                                                                                                                                                                                       745
745
745
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102
117
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1180
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205
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270
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                                                                                                                                                                 39947
                                                                                                  29.3%;
40.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GPCR_secretin
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                                                                                                                                                              MW;
                                                                             b; Score 629.5;
b; Pred. No. 1.2e
51; Mismatches
                                                                                                                                                                                                 CYTOPLASMIC (POTENTIAL).

6 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

7 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

BY SIMILARITY.

N-LINKED (GLCNAC. . . ) (PO'
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                                                                                                                                                                                                                                                                                                                                                                                            CYTOPLASMIC (
4 (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                     EXTRACELLULAR (POTENTIAL)
3 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CYTOPLASMIC (
2 (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EXTRACELLULAR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (POTENTIAL)
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                                                                             1.2e-36;
ches 130;
                                                                                                                                                                                                   (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (POTENTIAL).
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                                                                                                                        DВ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gonzalez-Roces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            В)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CXCR-2) (Fragment).
                                                                                                                 Length
                                                                               Indels
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                                                                                                                        353;
                                                                               31;
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                                                                               Gaps
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RESULT 8
II B_PANTR
ID ILBB_PA
AC Q28807)
DT 01-NOV
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Q28807;
01-NOV-1997 (Rel. 35, C
01-NOV-1997 (Rel. 35, I
01-NOV-1997 (Rel. 35, I
High affinity interleuk
     TRANSMEM
DOMAIN
TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                     EMBL; X91113; CAA62563.1; HSSP; P34996; 1DDD.
                                                                                                                                                                                                                                                                                                                                                                                                                                     the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                             DOMAIN
                                                                                                                                  Chemotaxis.
                                                                                                                                                                                                                                                             Pfam; PF00001; 7tm_1;
                                                                                                                                                                                                                                                                                  InterPro; IPR000276; GPCR_Rhodpsn.
InterPro; IPR000832; GPCR_secretin
                                                                                                                                                                                                                                                                                                                                                                                                                  or send
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Characterization of interleukin-8 receptors Immunogenetics 43:261-267(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alvarez V., Coto E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. MEDLINE-96175151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9598;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pan troglodytes (Chimpanzee).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IL8RB OR CXCR2
                                                                                                                                                                                     3-protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lopez-Larrea C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NEUTROPHILS CHEMOTACTIC FACTOR. BINDING OF 11-8 TO THE RECEPTOR CAUSES ACTIVATION OF NEUTROPHILS. THIS RESPONSE IS MEDIATED VIA A G-PROTEIN THAT ACTIVATE A PHOSEHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM. THIS RECEPTOR BINDS TO 11-8 WITH A HIGH AFFINITY AND TO GROWIGSA AND NAP-2 ALSO WITH A HIGH AFFINITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: Integral membrane protein. SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION: RECEPTOR TO INTERLEUKIN-8, WHICH IS A POWERFUL NEUTROPHILS CHEMOTACTIC FACTOR. BINDING OF IL-8 TO THE R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                                                                                                                                                                                                                                                  an email to license@isb-sib.ch).
                                                                                                                                                                             PS00237; G_PROTEIN_RECEP_F1_1; 1.
PS50262; G_PROTEIN_RECEP_F1_2; 1.
PS coupled receptor; Transmembrane;
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Rel. 35, Last annotation update)
interleukin-8 receptor B (IL-8R
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EXTRACELLULAR (POTENTIAL).
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                              STRAIN-ALBINO; TISSUE-Neutrophils; MEDLINE-91056034; PubMed=1700779; Thomas K.M., Pyun H.Y., Navarro J.; "Molecular cloning of the fMet-Leu-Ph J. Biol. Chem. 265:20061-20064(1990).
                                                                                                                                                                      Beckmann M.P., Munger W.E., Kozlosky C., Vandenbo
Lyman S., Gerard N.P., Gerard C., Cerretti D.P.,
"Molecular characterization of the interleukin 8
Biochem. Biophys. Res. Commun. 179:784-789(1991).
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Rel. 35, Last annotation update)
interleukin-8 receptor A (IL-8R
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Best Local S
Matches 136
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EMBL; M58021; AAA313
EMBL; M82873; AAA313
PIR; A23669; A23669.
                                                                             CONFLICT
SEQUENCE
                                                                                                 CONFLICT
                                                                                                                                                                                                   TRANSMEM
DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                              InterPro; TPR000276; GPCR_Rhodpsn.
InterPro; IPR000832; GPCR_secretin.
Pfam; PF00001; 7tm_1; 1.
PRINTS; PR00337; GPCRHODDPSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       J. Immunol. 148:1261-1264(1992)
-!- FUNCTION: RECEPTOR TO INTER
                                                                                                                                   CONFLICT
                                                                                                                                                                                                                                                         TRANSMEM
                                                                                                                                                                                                                                                                               TRANSMEM
                                                                                                                                                                                                                                                                                                     TRANSMEM
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PIR; JQ1231; JQ1231.
GCRDb; GCR_0107; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=92148149;
Lee J., Kuang W.-
                                                                                                                                                       CARBOHYD
                                                                                                                                                                    CARBOHYD
                                                                                                                                                                                                                                                                                                                                                          G-protein
                                                                                                                                                                                                                                                                                                                                                                                                                                 GCRDb; GCR_0108;
GCRDb; GCR_0298;
                                                                                                                                              DISULFID
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                                                                                                                                                                                                                                                                                                                                     DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                      PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Neutrophils;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IL-8 receptor."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lee J., Kuang W.-J., Rice G.C., Woo
Characterization of complementary
            69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: Integral membrane prote TISSUE SPECIFICITY: NEUTROPHILS.
SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN CAUTION: WAS ORIGINALLY (REF.2) THOUGHT TO BE FMET-LEU-PHE (N-FORMYL PEPTIDE RECEPTOR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RUNCTION: RECEPTOR TO INTERLEUKIN-8, WHICH IS A POWERFUL NEUTROPHILS CHEMOTACTIC FACTOR. BINDING OF IL-8 TO THE RECEPTOR CAUSES ACTIVATION OF NEUTROPHILS. THIS RESPONSE IS MEDIATED VIA G-PROTEIN THAT ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM.
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           NFSSSYDYGENESDSCCTSPPCPQDFS-----LNFDRAFLPALYSLLFLLGLLGNGAVA 122
                                  al Similarity
136; Conser
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                                                                                                                                                                                                                                                                                                                                                          coupled
                                                                          146
204
287
355
                                                                                                                                                                    Conservative
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115
90
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; AAA31377.1; -.
; AAA31376.1; -.
                                                                                                                                                                                                                                                                                                                                                                   G_PROTEIN_RECEP_F1_1;
G_PROTEIN_RECEP_F1_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PubMed=1737938;
                                                                                                                                                                                                                                                                                                                                                          receptor;
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67
73
114
138
159
184
2204
232
247
237
237
355
                                          28.6%;
                                                                             W.
                                 58;
                                                                                                                                                                                                            5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                         Transmembrane;
                                                                                      R -> C
DI ->
                                                                                                                                                                                                                                                                                                   EXTRACELLULAR (POTENTIAL)

1 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

2 (POTENTIAL).
                                           Pred.
                                                    Score 615.5;
                                                                                                                                BY SIMILARITY.
DLLFALTMPIWAVSKEKGWIFG
                                                                                                                                                     N-LINKED (GLCNAC. . .)
N-LINKED (GLCNAC. . .)
                                                                                                                                                                                                                                                         CYTOPLASMIC 4 (POTENTIAL
                                                                                                            PAFCPDHAYLGRLQGKRLDFR (IN HA -> QS (IN REF. 2).
                                                                                                                                                                             CYTOPLASMIC
                                                                                                                                                                                          EXTRACELLULAR (POTENTIAL)
7 (POTENTIAL).
                                                                                                                                                                                                                                  EXTRACELLULAR (POTENTIAL) 5 (POTENTIAL).
                                                                                                                                                                                                                                                                               EXTRACELLULAR (POTENTIAL)
3 (POTENTIAL).
                                                                         -> C (IN REF. 2).
[ -> EL (IN REF. 2).
EFE49ACB9D1E0F21 CF
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                                                                                                                                                                                                                                                                             (POTENTIAL)
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ary DNA clones encoding
                                 Mismatches
                                           No.
                                          1.1e-35;
                                                                                                                                                                             (POTENTIAL)
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RESULT 10
IL8B_RABIT
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                                                                                                         EMBL; L24445; PIR; A53752; F
                                                                                                                                                                                     use by non-profit institutions as long modified and this statement is not removed
                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                J. Biol. Chem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oryctolagus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    High affinity interleukin-8 receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation updat
                                          InterPro; IPR000276; GPCR_Rhodpsn.
InterPro; IPR000832; GPCR_secretin
Pfam; PF00001; 7tm_1; 1.
                                                                                                                                                       or send an email to license@isb-sib.ch).
                                                                                                                                                                        entities requires a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Folco E., N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P35344;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=94230294; PubMed=8175642;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=ALBINO; TISSUE=Blood;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IL8RB OR CXCR2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IL8B_RABIT
                                                                                                                                                                                                                                                                                                                                                                                                                                            sotype."
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Molecular characterization of a novel rabbit interleukin-8 receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               296
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                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: Integral membrane protein.
TISSUE SPECIFICITY: EXPRESSED PREFERENTIALLY IN NEUTROPHILS.
SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS
                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION: Integral membrane TISSUE SPECIFICITY: EXPRESSED PREFERENTI
                                                                                                                                                                                                                                                                                                                                                              FUNCTION: RECEPTOR TO INTERLEUKIN-8, WHICH IS A POWERFUL NEUTROPHILS CHEMOTACTIC FACTOR. BINDING OF IL-8 TO THE RECEPTOR CAUSES ACTIVATION OF NEUTROPHILS. THIS RESPONSE IS MEDIATED VIA G-PROTEIN THAT ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND
                                                                                                                                                                                                                                                                                                                                                 MESSENGER SYSTEM. THE AFFINITY OF THIS RECEPTOR IS IL-8 >>
                                                                                                                                                                                                                                                                                                                                    MGSA (GRO)
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                                                                                            GCR_0861;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cuniculus (Rabbit).
cuniculus (Rabbit).
Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
hitheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Thomas
                                                                                                           A53752.
                                                                                                                           AAA31378.1;
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                                                                                                                                                                      license agreement (See http://www.isb-sib.ch/announce/
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PROSITE;

G_PROTEIN_RECEP_F1_1;
G_PROTEIN_RECEP_F1_2;

Pfam; PF00001; 7tm_1; 1. PRINTS; PR00237; GPCRRHODOPSN

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Best Local S
Matches 141
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01-NOV-1997 (Rel. 35, L
01-NOV-1997 (Rel. 35, L
High affinity interleuk,
ILBRB OR CXCR2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chemotaxis.
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DOMAIN
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DOMAIN
       Lopez-Larrea C.;
"Characterization of interleukin-8 receptors Immunogenetics 43:261-267(1996).
-I- FUNCTION: RECEPTOR TO INTERLEUKIN-8, WHICE
                                               SEQUENCE FROM N.A. MEDLINE-96175151; Pul Alvarez V., Coto E.,
                                                                                                 Gorilla gorilla gorilla (Lowland gorilla).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae
                                                                                                                                                                        Q28422;
01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CARBOHYD
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                                                                                         NCBI_TaxID-9595
                                                                                                                                                                                           IL8B_GORGO
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hes 141;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ENFS-----SSYDYGENESDSCCTSPPCPQDFSLNFDRAFLPALYSLLFLLGLLGNG 119
                                                                                                                                                                                                                                                              GYMHCCLNPLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSSWSETS 408
                                                                                                                                                                                                                                                                                                                                    AVAAVLLSRRTALSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGLCKVAGALFN 179
                                                                                                                                                                                                                                                                                                                                                                                                                                               ENYSYEDFFGDFSNYSYSTDLPPTLLDSAPCRSE-SLETNSYVVLITYILVFLLSLLGNS
                                                                                                                                                                                                                                           GFLHSCLNPIIYAFIGQKFRYGLLKILAAHGLISKEFLAKESRPSFVASSSGNTS
                                                                                                                                                                                                                                                                                                                         NAIFPP--NSSPVCYEDMGNSTAKWRMVLRILPQTFGFILPLLVMLFCYVFTLRTLFQAH
                                                                                                                                                                                                                                                                                                                                                                VNFYSGILLLACISVDRYLAIVHATRTMIQKR---HLVKFICLSMWGVSLILSLPILLFR 182
                                                                                                                                                                                                                                                                                                                                                                            INFYAGALLLACISFDRYLNIVHATQ--LYRRGPPARVTLTCLAVWGLCLLFALPDFIFL
                                                                                                                                                                                                                                                                                  MGQKHRAMRVIFAVVLIFLLCWLPYNLVLLTDTLMRTHVIQETCERRNDIDRALDATEIL
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                                                                                                                                         interleukin-8 receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ą
                                                                                                                                                                                           STANDARD;
 CHEMOTACTIC
                                              PubMed=9110929;
E., Setien F., Gonzalez
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      46
73
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271
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313
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                40632
                                                                                                                                                    Last sequence update)
                                                                                                                                                                        Created)
INTERLEUKIN-8, WHICH IC FACTOR. BINDING OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ¥.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 1.26
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 615;
Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ВY
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N-LINKED (GLCNAC. . .)
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7 (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CYTOPLASMIC
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EXTRACELLULAR (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6899716944D6126A CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (POTENTIAL).
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                                                                                                                                         update)
B (IL-8R
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.2e-35;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (POTENTIAL).
                                                                                                  Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       139;
                             in non-human primates.";
                                                 Gonzalez-Roces
                                                                                                                                         B) (CXCR-2) (Fragment)
IL-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 358;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
TO THE RECEPTOR
                                                                                                            Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (POTENTIAL)
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                                                                                                  Gorilla
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                      TRANSMEM
DOMAIN
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TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NON_TER
                                                                                                                                                                                                                                                                                            SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; X91114; CAA62564.1; HSSP; P34996; 1DDD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or send an
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                                                                                                                                                                                                                                                                                                                                             RANSMEM
          303
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                                                                                                      ERLNATHCQYNFPQVG-----RTALRVLQLVAGFLLPLLVMAYCYAHILAVLLVSRGQR
        HSCLNPLIYAFIGORFCHGLLKILAIHGLISKDSLPKDSRPSFVGSSSGHT
                            HCCLNPLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSSWSET
                                                                  RLRAMRLVVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVTSGLGYM
                                                                                       SNVSPV-C---YEDMGNNTANWRMLLRILPQSFGFIVPLLIMLFCYGFTLRTLFKAHMGQ
                                                                                                                                         ISFDRYLNIVHATQLYRRGPPARVTLT------CLAVWGLCLLFALPDFIFLSAHHD
                                                                                                                                                                                        LSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGLCKVAGALFNINFYAGALLLAC 191
                                                                                                                                                                                                             SNYSYSSALPPFLLDASPCEPE-SLEINKYFVVIIYALVFLLSLLGNSLVILVILYSRVG
                                                                                                                                                                                                                              SSYDYGENESDSCCTSPPCPQDFSLNFDRAFLPALYSLLFLLGLLGNGAVAAVLLSRRTA 131
                                                                                                                              ISVDRYLAIVHATR------TLTQKRYLVKFICLSIWGLSLLLALPVLLFRRTIYP
                                                                                                                                                                     RSVTDVYLLNLALADLLFALTLPIWAASKVNGWIFGTFLCKVVSLLKEVNFYSGILLLAC
                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                         353
353
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205
228
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>353
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72
81
102
117
139
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                                                                                                                                                                                                                                                              28.5%;
39.3%;
                                                                                                                                                                                                                                                                                            WW;
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302

296 186 242 136

242

76

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PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; 1. PROSITE: PS50262; G_PROTEIN_RECEP_F1_2; 1. G-protein coupled receptor; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entities requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAUSES ACTIVATION OF NEUTROPHILS. THIS RESPONSE IS MEDIATED VIA A G-PROTEIN THAT ACTIVATE A PHOSPHATIDYLINOSTIOL-CALCIUM SECOND MESSENGER SYSTEM. THIS RECEPTOR BINDS TO IL-8 WITH A HIGH AFFINITY AND TO GRO, MUSA AND NAP-2 ALSO WITH A HIGH AFFINITY.

SUBCELLULAR LOCATION: Integral membrane protein.

SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the Swiss Institute of Bioinformatics
                                                                                                                                                                                                                                                                                                                                                                                                        IPR000276; GPCR_Rhodpsn. IPR000832; GPCR_secretin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            email to license@isb-sib.ch).
                                                                                               7 (POTENTIAL).
CYTOPLASMIC (PORTOPLASMIC)
BY SIMILARITY.
Score 614; DB 1; I
Pred. No. 1.4e-35;
2; Mismatches 131;
                                                                                N-LINKED
                                                                                                                             EXTRACELLULAR (POTENTIAL)
7 (POTENTIAL)
                                                                                                                                                         CYTOPLASMIC
6 (POTENTIAL
                                                                                                                                                                                                              CYTOPLASMIC
4 (POTENTIA)
                                                                                                                                                                                                                                                                   CYTOPLASMIC
2 (POTENTIAL
                                                                                                                                                                                              EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                   EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                            EXTRACELLULAR
                                                        1FF04E31A7E825E4 CRC64;
                                                                                                                                                      (POTENTIAL)
                                                                                                                                                                                 (POTENTIAL)
                                                                                                                                                                                                             (POTENTIAL)
                                                                                                                                                                                                                                        (POTENTIAL)
                                                                                                                                                                                                                                                                   (POTENTIAL)
                                                                                                                                                                                                                                                                                             (POTENTIAL)
                                                                                (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ormatics and the EMBL outstation
There are no restrictions on 19
you as its content is in no way
                                                                                                             (POTENTIAL)
                                                                                                                                                                                                                          (POTENTIAL).
                                                                                                                                                                   (POTENTIAL).
                                                                                                                                                                                                                                                                               (POTENTIAL).
                                                                                                                                                                                                                                                                                                       (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                 Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Usage
                           Length 353;
  Indels
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RESULT 12
IL8A_GORGO
  Query Match
Best Local S
Matches 136
                                                                              DOMAIN
CARBOHYD
                                                                                                                                                                                                    TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gorilla gorilla (Lowland gorilla), and Pongo pygmaeus (Orangutan).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; lammmalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
High_affinity_interleukin-8 receptor A (IL-8R A) (IL-8 receptor type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P55919;
                                                        DISULFID
                                                                                                    TRANSMEM
                                                                                                                                                                                                                                                          Chemotaxis.
                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Characterization of interleukin-8 receptors in non-human primat Immunogenetics 43:261-267(1996).

-i- FUNCTION: RECEPTOR TO INTERLEUKIN-8, WHICH IS A POWERFUL NEUTROPHILS CHEWOTACTIC FACTOR. BINDING OF IL-8 TO THE RECEPTOR TO THE RESPONSE IS MEDIATED CAUSES ACTIVATION OF NEUTROPHILS. THIS RESPONSE IS MEDIATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alvarez V., Coto E.,
Lopez-Larrea C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. MEDLINE=96175151;
                                                                                                                           TRANSMEM
                                                                                                                                     DOMAIN
                                                                                                                                               TRANSMEM
                                                                                                                                                            DOMAIN
                                                                                                                                                                               DOMAIN
                                                                                                                                                                                           TRANSMEM
                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                         PROSITE;
                                                                                                                                                                                                                                                                                                     PRINTS; PR00237; GPCRRHODOPSN.
                                                                                                                                                                                                                                                                                                                                                           EMBL; X91110;
                                                                                                                                                                                                                                                                                                                                                                               or send an email to license@isb-sib.ch).
                                                                                                                                                                     TRANSMEM
                                                                                                                                                                                                                                     TRANSMEM
                                                                                                                                                                                                                                                                   3-protein
                                                                                                                                                                                                                                                                                PROSITE;
                                                                                                                                                                                                                                                                                                               Pfam; PF00001; 7tm_1;
                                                                                                                                                                                                                                                                                                                        InterPro; IPR000276; GPCR_Rhodpsn.
InterPro; IPR000832; GPCR_secretin
                                                                                                                                                                                                                                                                                                                                                HSSP; P25024;
                                                                                                                                                                                                                                                                                                                                                                                                                                      between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9595, 9600;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IL8RA OR CXCR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IL8A_GORGO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CXCR-1)
                                                                                                                                                                                                                                                                                                                                                                                                                         European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               AND TO MGSA (GRO) WITH A LOW AFFINITY.
SUBCELLULAR LOCATION: Integral membrane protein.
SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    G-PROTEIN THAT ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM. THIS RECEPTOR BINDS TO IL-8 WITH A HIGH AFFINITY
                                                                                                                                                                                                                                                                                                                                                                                                                                  SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN
   al Similarity
136; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P55921;
                                                                                                                                                                                                                                                                                                                                                                                                   non-profit institutions as long and this statement is not removed
                                                                                                                                                                                                                                                                              PS00237; G_PROTEIN_RECEP_F1_1; PS50262; G_PROTEIN_RECEP_F1_2;
                                                                                                                                                                                                                                                                      coupled
                                             350
                                                       (CDW128).
   Conservative
                                                                                                                                                                                                                                                                                                                                                           CAB37671.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PubMed=9110929;
                                                                                                                                                                                                                                                                     receptor;
                                                       39790
           28.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Setien
                                             MW;
   50;
                                                                                                                       5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         - F.,
                                                                                                                                                                                                                                                                     Transmembrane;
           Score 612.5;
Pred. No. 1.1
                                                              CYTOPLASMIC (POTENTIAL).

-LINKED (GLCNAC. . .) (POTENTIAL)

-LINKED (GLCNAC. . .) (POTENTIAL)
                                                        ВΥ
                                                                                                                                                                              3 (POTENTIAL)
CYTOPLASMIC (
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2 (POTENTIA
                                                                                                                                                      4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
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                                            DB99591CD6C10757 CRC64;
                                                                                                    (POTENTIAL)
                                                                                                                                                                                                              (POTENTIAL)
                                                                                                                                                                                                                                    (POTENTIAL)
  Mismatches
                                                        SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gonzalez S.,
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            1.8e-
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                                                                                                                                                                             (POTENTIAL).
                                                                                                                                                                                                                        (POTENTIAL).
                                                                                                                                 (POTENTIAL).
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                        DΒ
                                                                                                                                                                                                                                                                     Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gonzalez-Roces
                                                                                                                                                                                                                                                                                                                                                                                                   Usage
                      1;
                      Length
  Indels
                                                                                                                                                                                                                                                                                                                                                                                                    γď
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Euteleostomi;
Gorilla.
                                                                                                                                                                                                                                                                                                                                                                                                                         restrictions
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                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL
                        350;
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 31;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      collaboration -
L outstation -
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Gaps
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IL8B_BOVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IL8B_BOVIN STAN
Q28003;
01-NOV-1997 (Rel. :
01-NOV-1997 (Rel. :
01-NOV-1997 (Rel. :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bos taurus (Bovine).
Eukaryota; Metazoa; C
Mammalia; Eutheria; C
Bovidae; Bovinae; Bos
                                                                                                                                                              rinerpro; IPRO00276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
PRINTS; PRO0007
                                                                                                                                                                                                                                                                                                                         modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                            Chemotaxis
DOMAIN
                                                                            G-protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Li V., Feng J., Templeton J.W.;
Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases
-i- FUNCTION: RECEPTOR TO INTERLEUKIN-8, WHICH IS A POW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        High affinity
                                                                                                           PROSITE; PS00237; G_PROTEIN_RECEP_F1_1;
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2;
                                                                                                                                                                                                                                                                            EMBL; U19947; AAA84996.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                        the European Bioinformatics Institute.
  TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: Integral membrane protein.
SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               G-PROTEIN THAT ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM. THIS RECEPTOR BINDS TO IL-8 WITH A HIGH AFF. AND TO GRO/MGSA AND NAP-2 ALSO WITH A HIGH AFFINITY (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION: RECEPTOR TO INTERLEUKIN-8, WHICH IS A POWERFUL NEUTROPHILS CHEMOTACTIC FACTOR. BINDING OF IL-8 TO THE RECEPTOR CAUSES ACTIVATION OF NEUTROPHILS. THIS RESPONSE IS MEDIATED VIA A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SWISS-PROT entry is copyright. It is produced through a \circ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSSWSETS
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  49
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Rel. 35, Last sequence update)
Rel. 35, Last annotation update)
interleukin-8 receptor B (IL-8R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
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                                                                                  Transmembrane;
EXTRACELLULAR (POTENTIAL)
1 (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                           There are no rest
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                                                                                  Glycoprotein;
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IL8A_HUMAN
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Best Local S
Matches 141
                                                                                                            P25024;
P25024;
01-MAY-1992 (Rel. 22, Creace,
01-MAY-1992 (Rel. 22, Last sequence update,
16-OCT-2001 (Rel. 40, Last annotation update)
7-4 Affinity interleukin-8 receptor A (IL-8R
receptor.
Science 2
[2]
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DOMAIN
                                         SEQUENCE FROM N.A. MEDLINE=91368199;
                                                                         Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
MCBI_TaxID=9606;
                                                                                                       Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                        Holmes W.E., Le "Structure and "
                                                                                                                                                                                  IL8A_HUMAN
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                                                                                                      sapiens (Human).
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                                                                                                                                                                                                                                  SSSGNTS
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                                                                                                                                                                                                                                                                                                                    YAHILAVLLVSRGQRRLRAMRLVVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRES
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                                                                                                                                                                                                                                                                                       RYDVAKSVTSGLGYMHCCLNPLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRD
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         253:1278-1280(1991):
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                                     Lee J.,
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                           functional expression
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                                                                                                                                                                                 STANDARD;
                                     PubMed=1840701;
J., Kuang W.-J.,
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CYTOPLASMIC (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
BY SIMILARITY
N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . . .) (POTENTIAL)
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6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
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Pred. No. 5.
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3 (POTENTIAL).
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2 (POTENTIAL).
                                                                                   Craniata; Vertebrata; Catarrhini; Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9A7F70C982A632D1 CRC64;
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                           Rice (
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                            human
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                                     Wood
                                                                                                                                  A) (IL-8
                           interleukin-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 360;
                                     W. I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                            Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                      -CLAVWGLCLLF
                                                                                                                                  receptor type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42;
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Lee J., Horuk R., Rice G.C., Bennett G. "Characterization of two high affinity receptors.";
                                                                                                                                                                                                                      Structure 7:157-168(1999).
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MEDLINE=93252387; PubMed=8486366;

MOllereau C., Passage E., Mattei M.-G., Vassart G., Parmentier

"The high-affinity interleukin 8 receptor gene (IL8RA) maps to
2433-436 region of the human genome: cloning of a pseudogene
(IL8RBP) for the low-affinity receptor.";

Genomics 16:248-251(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GRO/melanoma growth-stimulatory
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Beckmann M.P.;
"Molecular characterization of
                                                                                                                                                                                                                                                                             Skelton N.J., Quan C
"Structure of a CXC
                                                                                                                                                                                                                                                                                                            MEDLINE=99148123; PubMed=10368283; Skelton N.J., Quan C., Reilly D.,
                                                                                                                                                                                                                                                                                                                                                            STRUCTURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ahuja S.K., Shetty A., Tiffany H.L., Muri
"Comparison of the genomic organization of
human interleukin-8 receptors A and B.",
J. Biol. Chem. 269:26381-26389(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=95014476; PubMed=7929358; Ahuja S.K., Shetty A., Tiffany H.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=93205012; PubMed=8384312;
Cerretti D.P., Kozlosky C.J., Van
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                      interleukin-8.
                                                                                                                                                                                                                                                                                                                                                                                    6
FUNCTION: RECEPTOR TO INTERLEUKIN-8, WHICH IS A POWERFUL NEUTROPHILS CHEMOTACTIC FACTOR. BINDING OF IL-8 TO THE RECEPTOR CAUSES ACTIVATION OF NEUTROPHILS. THIS RESPONSE IS MEDIATED VIA A G-PROTEIN THAT ACTIVATE A PHOSPHATIDVLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM. THIS RECEPTOR BINDS TO IL-8 WITH A HIGH AFFINITY AND TO MGSA (GRO) WITH A LOW AFFINITY.

SUBCELLULAR LOCATION: Integral membrane protein.

SUBCELLULAR LOCATION: TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

SUBCELLULAR LOCATION: NOTE-CD guide CDw128a entry:

DATABASE: NAME-PROW; NOTE-CD guide CDw128a htm.
                                                                                                                                                                                                                                                                                                                                                                                                          Chem.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N.A.
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MIM; 15.
InterPro; 15.
"am; PF00001; " EMBL; L19591; AAB59436.1; -EMBL; L19592; AAA59160.1; -EMBL; M68932; AAA59159.1; -EMBL; X65858; CAA46688.1; -EMBL; U11870; AAA6378.1; -PIR; A39445; A39445. PDB; 1ILP; 23-DEC-98.
PDB; 1ILQ; 23-DEC-98.
GCRDb; GCR_0175; -GCRDb; GCR_0696; -GCRDb; GCR_1832; -GCRDb; GCR_1832; -GCRDb; GCR_2052; -use by non-profit institutions as long as its cont modified and this statement is not removed. Usage by entitles requires a license agreement (See http://www.or send an email to license@isb-sib.ch). This between European Bioinformatics Institute. SWISS-PROT entry is copyright. It is produced through a collaboratic en the Swiss Institute of Bioinformatics and the EMBL outstation IPR000276; There are no restrictions on ong as its content is in no .isb-sib and for collaboration -L outstation -.ch/announce,

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RESULT 15
IL8B_RAT
ID IL8B_RAT
ID IL8B_RAT
ID IL8B_RAT
ID IL9B_RAT
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Best Local
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                                                                                                                                                                             IL8B_RAT
P35407;
01-JUN-1994
01-FEB-1996
30-MAY-2000
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CARBOHYD
DISULFID
VARIANT
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                                                                                                                                                           01-JUN-1994 (Rel. 29, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
High affinity interleukin-8 receptor B (IL-8R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   G-protein
                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                    Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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   SEQUENCE FROM N.A.
STRAIN=SPRAGUE-DAWLEY;
                                                     NCBI_TaxID=10116;
                                                                                                                           receptor).
IL8RB OR CXCR2.
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                                                                                                                                                                                                                                                                                                                                          GQNFRHGFLKILAMHGLVSKEFLARHRVTSYTSSSVNVSS
                                                                                                                                                                                                                                                                                                                                                                           GVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSSWSETS
                                                                                                                                                                                                                                                                                                                                                                                                                                 PPCPQDFS-----LNFDRAFLPALYSLLFLLGLLGNGAVAAVLLSRRTALSSTDTFLLH
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                                                                                                                                                                                                                                                     STANDARD;
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TISSUE-Lung;
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N-LINKED (GLCNA
N-LINKED (GLCNA
BY SIMILARITY.
T -> S.
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EXTRACELLULAR (POTENTIAL)

5 (POTENTIAL)
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Pred. No. 5.4
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7 (POTENTIAL)
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6 (POTENTIA)
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2463EEB51BEDD039 CRC64;
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3 (POTENTIAL).
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2 (POTENTIA
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                                                                    Sciurognathi;
                                                                                                                                                                                                                                                     PRT;
                                                                                        Craniata; Vertebrata; Euteleostomi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (POTENTIAL)
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(GLCNAC. . .) (I
                                                                                                                                                                                                                                                     359
                                                                                                                                                              (IL-8R
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                                                                        Muridae;
                                                                                                                                                                                                                                                                                                                                          348
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TRANSMEM
DOMAIN
CARBOHYD
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DOMAIN
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J. Biol. Chem. 271:32770-32776(1996).
J. Biol. Chem. 271:32770-32776(1996).
I. FUNCTION: RECEPTOR TO INTERLEUKIN-8, WHICH IS A POWERFUL NEUTROPHILS CHEMOTACTIC FACTOR. BINDING OF IL-8 TO THE RECEPTOR CAUSES ACTIVATION OF NEUTROPHILS. THIS RESPONSE IS MEDIATED VIA G-PROTEIN THAT ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM. THIS RECEPTOR BINDS TO IL-8 WITH A HIGH AFFINITY.

AND TO GRO/MGSA AND NAP-2 ALSO WITH A HIGH AFFINITY.
DISULFID SEQUENCE
                                                                                                                                                                                                                                                                                                            DOMAIN
TRANSMEM
                                                                     CARBOHYD
                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                   Chemotaxis
                                                                                                                                                                                                                                                                                                                                                                                                    G-protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCRDb; GCR_1524; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCRDb;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; X77797; EMBL; D63584;
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or send an
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MEDLINE-97115810; PubMed-8955112;
Dunstan C.-A.N., Salafranca M.N., Adhikari S.,
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Gobl A.E., Huang M.R., Wang S., Zhou Y., Oe
"Molecular cloning and characterization of
interleukin-8 receptor.";
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GCR_1405; -
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186 VKANPSTVVCYEN---IGNNTSKWRVVLRILPQTYGFILLPLLIMLFCYGFTLRTLFKAHM 242
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Search completed: November 2, 2002, 12:05:23 Job time : 28 secs

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01-0CT-2001 (TremBLrel. 15, L
01-0CT-2001 (TremBLrel. 18, L
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PROSITE; F
Receptor.
SEQUENCE
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"Identification and molecular characterization of rat CXCR3: receptor
expression and interferon-inducible protein-10 binding are increased
                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                              Mol. Pharmacol. 57:1190-1198(2000).
EMBL; AF223642; AAF76982.1; -
InterPro; IPR004070; CXCchemok_receptor3.
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
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PRINTS; PR00237; GPCRRHODOPSN.

PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.

PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
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MEDLINE=20286573; Pubmed=10825390;
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Similarity
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                                                       76.2%; score 1638.5; DB 1
86.3%; Pred. No. 1.4e-138;
tive 23; Mismatches 26;
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Matches 315; Conser
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                                                                                                                                                                                                                                                                                                                                                Receptor.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MUS musculus (Mouse).
Mus musculus (Mouse).
'``rvota; Metazoa; Chordata;
'`rvota; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR01532; CXCCHMKINER3.

PRINTS; PR00237; GPCRRHODOPSN.

PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1

PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
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InterPro; IPR004070; CXCchemok_receptor3.

InterPro; IPR000276; GPCR_Rhodpsn.

Pfam; PF00001; 7tm_1; 1.
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                                                                                           FLLGLLGNGAVAAVLLSRRTALSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGL
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hing of the murine interferon-inducible protein 10 (IP-10)
tor and its specific expression in lymphoid organs.";
em. Biophys. Res. Commun. 251:41-48(1998).
AB003174; BAA34045.1; -.
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86.3%;
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Pred. No. 8.9e
21; Mismatches
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Best Local S
Matches 133
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Gallus gallus (Chicae Bukaryota; Metazoa; (Chicae Bukaryota; Metazoa; (Chicae Bukaryota; Aves; N
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093281;
01-NOV-1998
                                                                                                                                                                                                                                                                                                                                      Receptor.
SEQUENCE
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EMBL; AF029369; AAC23950.1; -

InterPro; IPR000276; GPCR_Rhodpsn.

Pfam; PF00001; 7tm.1; 2.

PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                              stage chick embryos."
Biochem. Mol. Biol. I
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Gupta S.K., Pillarisetti K., Gray S.L.,
"Molecular cloning of a novel chemokine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1998
01-DEC-2001
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            GYMHCCLNPLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSSWSETSEASYS
                                                                                     WTDES-NRSICY--FPEAGIHGNNVWLATRFLYHSVGFFMPLLVMCYCYMAIVRTLCQSQ
                                                                                                HHDERLNATHCQYNFPQVG-----RTALRVLQLVAGFLLPLLVMAYCYAHILAVLLVSR 293
                                                                                                                                                    INFYAGALLLACISFDRYLNIVHATQLYRRGPPARVTLTCLAVWGLCLLFALPDFIFLSA 239
                                                                                                                                                                                                              AVAAVLLSRTALSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGLCKVAGALFN 179
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133; Conserv
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Q9MZM7;

01-OCT-2000 (TrEMBLrel. 15,

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O1-OEC-2001 (TrEMBLrel. 19,

O1-OEC-2001 (TrEMBLrel. 19,
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Q9DGI1;
01-MAR-2001
01-MAR-2001
01-DEC-2001
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Pfam; PF00001; 7tm_1; 1.

PRINTS; PR00237; GPCRHODOPSN.

PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.

PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.

PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.

G-protein coupled receptor; Glycoprotein; Receptor;

G-protein coupled receptor; Glycoprotein; Receptor;

SEQUENCE 358 AA; 40094 MW; 64E4977E29C86C9E CRC6
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J. Leukoc. Biol. 69:297-305(2001).

-I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).

-I- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAKFKTSAQNALTSVSRGSSLKILSKSKRGGHSSVSTESESSSF
                                                                                                                                                                                                                                           GVKFRERMWMLL------LRLGCPNQRGLQRQPSSSRRDSSW
                                                                                                                                                                                                                                                                                                     SSSY-DYGENESDSCCTSPPCPQDFSLNFDRAFLPALLYSLLFLLGLLGNGAVAAVLLSRR 129
                                                                                                                                                                                                                                                                                                                                                    CDRMYPHDNWLISFRFQHILVGLVLPGLIILTCYCIIISKLSHSKGHQKRKALKTTVILI 251
                                                                                                                                                                                                                                                                                                                                                                                                                            AFISLDRYLAIVHATNSORPRKLLAEKIVYVGVWLPAVLLTVPDIIFASTSEVE--GRYL 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                ACISFDRYLNIVHATQLYRRGPPARVTLTCLAVWGLCLLFALPDFIFLSAHHDERLNATH
                                                                                                                                                                                                                                                                              LTFFACWLPYYIGISIDTFILLGVIRHRCSLDTIVHKWISITEALAFFHCCLNPILYAFL
                                                                                                                                                                                                                                                                                                                                                                                        CQYNFPQVG-RTALRVLQLVAGFLLPLLVMAYCYAHILAVLLVSRGQRRLRAMRLVVVVV 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SADYGDYGE-----PCFQHENADFNRIFLPTIYSIIFLTGIIGNGLVIIVMGYQK 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GFTHCCLNPIIYAFIGVKFRNDFFRILHELGCISQETLQEILEVTRKGCGIESDNTTSIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (TrEMBLrel. 16, (TrEMBLrel. 16, 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PubMed=11272281;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Chordata;
Neognathae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27.2%; Score 585; DB 13; 35.8%; Pred. No. 2.8e-44;
                                         15, Created)15, Last sequence update)19, Last annotation updat
                              (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          s.,
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Last annotation updat
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; Galliformes; Phasianidae; Phasianinae;
                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches 134;
                                                                                                                    347
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                                           update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
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                                                                                                                                                                                                           355
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Best Local S
Matches 122
                                                                                                                                                                                                                                                                                               093237
093237;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9495;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                            299
                                                                                                                                                                                                                                                                                                                                                                                                                                            367
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       128
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Fujiki K., Shin D., Nakao M., Yano T.;
"Molecular cloning of carp (Cyprinus carpio)
chemokine receptors, allograft inflammatory
                                                                                                                                                                                                                                         01-NOV-1998 (TrEMBLrel. 0
01-NOV-1998 (TrEMBLrel. 0
01-DEC-2001 (TrEMBLrel. 1
CXC CHEMOKINE RECEPTOR-1.
                                                                                                                                 Eukaryota; Métazoa; Chordata; Craniata;
Actinopterygii; Neopterygii; Teleostei;
Cypriniformes; Cyprinidae; Cyprinus.
CYPTINIGET CYPTINIGET CYPTINUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Callimico goeldii (Goeldi's marmoset).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Callimico
                                                          SEQUENCE FROM N.A.
MEDLINE=99367403; PubMed=10436187;
                                                                                                                                                                                                                    Cyprinus carpio (Common carp).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1;
PROSITE: PS50362; G_PROTEIN_RECEP_F1_2;
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000276; GPCR_Rhodpsn.
InterPro; IPR003006; Ig_MHC.
Pfam; PF00001; 7tm_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SUBCELLULAR LOCATION: INTEGRAL N
-!- SIMILARITY: BELONGS TO FAMILY 1
EMBL; AF172236; AAF89356.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (JUL-1999) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Theng X.-Z., Zhang Y.
Molecular Evolution
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          THCQYNFP-QVGRTALRVLQLVAGFILPLLVMAYCYAHILAVLLVSRGQRRLRAMRLVVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKTTVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LLACISFDRYLNIVHATQLYRRGPPARVTLTCLAVWGLCLLFALPDFIFLSAHHDERLNA 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FVGVKFRERMWMLL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LILAFFACWLPYYIGISIDSFILLEIIRQGCEFENTVHKWISITEALAFFHCCLNPILYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVTSGLGYMHCCLNPLLYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIF--ANVSEADDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QKKLRSMTDKYRLHLSVADLLLVITLPFWAVDAVANWYFGKFLCKAVHVIYTVNLYSSVL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RRTALSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGLCKVAGALFNINFYAGAL 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNYTEEMGSGDYDS----IKEPCFREENAHFNRIFLPTIYSIIFLTGIVGNGLVILVMGY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  347 AA;
                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  39269 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26.8%;
                                                                                                                                                                                                                                                             08,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -LRLGCPNQRGLQRQPSSSRRDSSW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 577.5; |
Pred. No. 1.3e
69; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL/GenBank/DDBJ databases.
NTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
                                                                                                                                                                                                                                                                Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                             Created)
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                                                                                                                                                                                                                                                                                                                                                        372
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                                                                                                                                                                            Vertebrata;
Euteleostei;
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  ) CC chemok factor-1,
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                        chemokine,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         404
                                                                                                                                                                                                  Euteleostomi;
                                                                                                                                                                            Ostariophysi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15;
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Best Local Sim
Matches 134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro: IPRO00276; GPCR_Rhodpsn.

Pfam; PF00001; 7tm_1; 1.

PRINTS; PR00237; GPCRRHODDPSN.

PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.

PROSITE; PS00237; G_PROTEIN_RECEP_F1_2; 1.

PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.

G-protein coupled receptor; Glycoprotein; Recept G-protein coupled receptor; Glycoprotein coupled receptor; Glycoprotein coupled receptor; G-protein coupled receptor; G
                                                                                        Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY)
-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9MZN6;
01-OCT-2000
-i- SUBCELLULAR LOCATION: INTEGRAL N-i- SIMILARITY: BELONGS TO FAMILY 1
EMBL; AF172227; AAF89347.1; -
InterPro; IPR000276; GPCR_Rhodpsn.
InterPro; IPR003006; Ig_MHC.
Pfam; PF00001; 7tm_1; 1.
                                                                                                                                                                                             Zheng X.-Z., Zhang Y. Molecular Evolution
                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla; Eutheria; Primates; Catarrhini; Hylobatid;
                                                                                                                                                                                                                                                                                                                                                                      Hylobates concolor leucogyneus
                                                                                                                                                                                                                                                                                                                                                                                                  CXCR4
                                                                                                                                                                                                                                                                                                                                                                                                                    01-CCT-2000 (TrEMBLrel. 15, Created)
01-CCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation updat
CHEMOKINE RECEPTOR CXCR4 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9MZN6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -: SUBCELLULAR LOCATION: INTEGRAL
-: SIMILARITY: BELONGS TO FAMILY
EMBL, ABOLJ0468; BAA31458.1; -.
HSSP; P34996; IDDD
                                                                                                                                                                         Primates.";
                                                                                                                                                                                                                                                                                               NCBI_TaxID=101280;
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FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut
Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae;
NCBI_TaxID=61851;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation updat
CHEMOKINE RECEPTOR CXCR4 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                      Q9MZN5;
                                                                         PRINTS: PR00237; GPCRRHODOPSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1;
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2;
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
G-protein coupled receptor; Glycoprotein
                                                                                                                                        InterPro; IPR000276; GPCR_Rhodpsn.
InterPro; IPR003006; Ig_MHC.
Pfam; PF00001; 7tm_1; 1.
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                                                               G-protein
NON_TER
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                                                                                                                                                                                                                                                                            SEQUENCE
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PROSITE; PS00237; G_PROTEIN_RECEP_F1_1;
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2;
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
                                                                                                                                                                                            -i- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY)
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70;
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Pred. No. 1.0
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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InterPro; IPR003006; Ig_MHC.
Pfam; PF00001; 7tm_1; 1
PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1;
PROSITE; PS00237; G_PROTEIN_RECEP_F1_2;
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
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-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY)
-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane NON_TER 1
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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SEQUENCE 347 AA; 39209 MW; D853326462E15B22 CRC64;
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-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
CHEMOKINE RECEPTOR CXCR4 (FRAGMENT).
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InterPro; IPR003006; Ig_MHC.
Pfam; PF00001; 7tm_1; 1.
PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1;
PROSITE; PS00237; G_PROTEIN_RECEP_E1_2;
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SUBCELLULAR LOCATION: INTEGRAL N
-!- SIMILARITY: BELONGS TO FAMILY 1
EMBL; AF172232; AAF89352.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zheng X.-Z., Zhang Y.-P., Geng Z.-C.;
"Molecular Evolution of the Chemokine Receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gorilla gorilla (gorilla)
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                                                                                                         VVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVTSGLGYMHCCLNPLLYA 366
                                                                                                                                                                                                                      THCQYNFP-QVGRTALRVLQLVAGFLLPLLVMAYCYAHILAVLLVSRGQRRLRAMRLVVV
                                                                                                                                                                                                                                                                                                              LLACISFDRYLNIVHATQLYRRGPPARVTLTCLAVWGLCLLFALPDFIFLSAHHDERLNA 247
                                                                                                                                                                                                                                                                                                                                                                                        RRTALSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGLCKVAGALFNINFYAGAL 187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ENFSSSYDYGENESDSCCTSPPCPQDFSLNFDRAFLPALYSLLFLLGLLGNGAVAAVLLS 127
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                                                       LILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPILYA
                                                                                                                                                                 YICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKTTVI
                                                                                                                                                                                                                                                                              ILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIF--ANVSEADDR 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSF 344
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- LRLGCPNQRGLQRQPSSSRRDSSW
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Pred. No. 1.6e-43;
0; Mismatches 140;
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Best Local :
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     Q9MZM1;
01-OCT-2000
01-OCT-2000
01-DEC-2001
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PROSITE; PS00237; G_PROTEIN_RECEP_F1_1;
PROSITE; PS050862; G_PROTEIN_RECEP_F1_2;
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -i- SUBCELLULAR LOCATION: INTEGRAL MEME-i- SIMILARITY: BELONGS TO FAMILY 1 OF EMBL; AF172235; AAF89355.1; -
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Mammalia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (JUL-1999) to the
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InterPro; IPR003006; Ig_MHC.
Pfam; PF00001; 7tm_1; 1.
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                                                                                                                                                                                                        YAFVGVKFRERMWMLL-----LRLGCPNQRGLQRQPSSSRRDSSW
                                                                                                                                                                                                                                            VILILAFFACWLPYYIGISIDSFILLEIIRQGCEFENTVHKWISITEALAFFHCCLNPIL
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                                                                                                                                                                                                                                                                                                                                                                                                                              LLACISFDRYLNIVHATQLYRRGPPARVT--LTCLAVWGLCLLFALPDFIFLSAHHDERL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGKFLCKAVHVIYTVNLYSSVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNYTEEIGSGDYDS----IKEPCFREENAHFNRIFLPTIYSIIFLTGIVGNGLVILVMGY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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   ) (TrEMBLrel.) (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          347 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                              PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Y.-P., Geng Z.-C.;
on of the Chemokine Receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          39152 MW;
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15, Last sequence update)
19, Last annotation updat
     15,
15,
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Created)
Last sequence update)
Last annotation update)
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NTEGRAL MEMBRANE PROTEIN (BY SIMILARITY)
FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 576.5;
Pred. No. 1.6
                                                                              PRT;
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Best Local
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                                                                                                                                                  O9MZP6
O9MZP6;
O9MZP6;
O1-OCT-2000 (TrEMBLrel. 15, Created)
O1-OCT-2000 (TrEMBLrel. 15, Last sequence update)
O1-DEC-2001 (TrEMBLrel. 19, Last annotation updat
                                                                                                            Eukaryota;
Mammalia; E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro;
Pfam; PF0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.

NON_TER 1 1
SEQUENCE 347 AA; 39155 MW; 9BFA91A3824F7A7A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PRO0237; GPCKRHODOPSN.

PROSITE; PS00237; G_PROTEIN_RECEP_F1_1;

PROSITE; PS50262; G_PROTEIN_RECEP_F1_2;

PROSITE; PS00290; IG_MHC; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHEMOKINE RECEPTOR CXCR4 (FRAGMENT).
                                                                          NCBI_TaxID=98375;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Primates."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=30602;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Strepsirhini; Lemuridae; Eulemur.
 Zheng X.-Z., Zhang Y.
"Molecular Evolution
                                      SEQUENCE FROM
                                                                                             Presbytis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zheng
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eulemur macaco (Petterus macaco)
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"Molecular Evolution
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                                                                                                                                                                                                                                                                                                                                                                                                              AFVGVKFRERMWMLL-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LLACISFDRYLNIVHATQLYRRGPPARVTLTCLAVWGLCLLFALPDFIFLSAHH-DERLN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pro; IPR000276; GPCR_Rhodpsn.
Pro; IPR003006; Ig_MHC.
PF00001; 7tm_1; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  al Similarity 35.7
122; Conservative
                                                                                                              i; Metazoa;
Eutheria;
                                        N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        on of
                                                                                                              Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Cercopithecidae; Colobi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26.8%;
   of
 the Chemokine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ., Geng Z.-C.; the Chemokine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    68;
                                                                                                                                                                                                                                                                                                                                                                                                           LRLGCPNQRGLQRQPSSSRRDSSW
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Pred. No. 1.6e-43;
8; Mismatches 140;
                 Z.-C.;
 Receptor CXCR4 Gene
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404

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RESULT 14
Q9MZP2
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Best I
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            -!- SUBCELLULAR LOCATION: INTEGRAL MEM-
-!- SIMILARITY: BELONGS TO FAMILY 1 OF
EMBL; AF172221; AAF89341.1;
InterPro; IPR000276; GPCR_Rhodpsn.
InterPro; IPR00306; Ig_MHC.
Pfdm; PF00001; 7tm_1; 1.
PRINTS; PR00237; GPCRRHODOPSN.
                                                                                                                                                                                                                                                                                Q9MZP2
Q9MZP2;
01-OCT-2000
01-OCT-2000
01-DEC-2001
    PRINTS;
PROSITE;
                                                                                                                                                                                                 Mandrillus sphinx (Mandrill) (Papio sphinx).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithe
Cercopithecinae; Mandrillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPRO00276; GPCR_Rhodpsn.
InterPro; IPRO03006; Ig_MHC.
Pfam; PF00001; 7tm.1; 1.
PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1;
PROSITE; PS00239; G_PROTEIN_RECEP_F1_2;
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
                                                                                                       Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                        Primates.";
                                                                                                                                   Zheng X.-Z., Zhang Y.
Molecular Evolution
                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                     Cercopithecinae;
NCBI_TaxID=9561;
                                                                                                                                                                                                                                                                    CHEMOKINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane NON_TER 1 1
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-!- SIMILARITY: BELONGS TO
EMBL; AF172217; AAF89337.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVTSGLGYMHCCLNPLLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATHCQYNFF-QVGRTALRVLQLVAGFLLPLLVMAYCYAHILAVLLVSRGQRRLRAMRLVV
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                                                                                                                                                                                                                                                                                                                                                                                                    AFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSF
                                                                                                                                                                                                                                                                                                                                                                                                                             AFVGVKFRERMWMLL-----LRLGCPNQRGLQRQPSSSRRDSSW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --ICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKTTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ILASISLDRYLAIVHATNSQKPRKLLAEKVVYVGVWIPALLLTIPDFIFASVSEADDRY-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                 00 (TrEMBLrel. 15, Created)
00 (TrEMBLrel. 15, Last sequence update)
01 (TrEMBLrel. 19, Last annotation update)
RECEPTOR CXCR4 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (JUL-1999) to the EMBL/GenBank/DDBJ databases.
LLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY)
ARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               347 AA; 39145 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
G_PROTEIN_RECEP_F1_1;
                                                                                                                                   y Y.-P., Ge
lon of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26.8%;
                                                                                                                                   Geng Z.-C.;
he Chemokine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 575.5;
Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             D21B7BB4AF3DF693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                              MEMBRANE PROTEIN (BY SIMILARITY)
1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                     347
                                                                                                                                Receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .9e-43;
                                                                                                                                                                                                            Cercopithecidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          138;
                                                                                                                                                                                                                                                                                update)
                                                                                                                                  CXCR4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CRC64;
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                                                                                                                                                                                                                           Euteleostomi;
                                                                                                                                  Gene
                                                                                                                                                                                                                                                                                                                                                                                                                             404
                                                                                                                                  Sequences
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RESULT 15
Q9MZM6
ID Q9MZM
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                                                                                                                                                                                                                                                              -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PEMBL; AF172237; AAF89357.1; -
InterPro; IPR000276; GPCR_Rhodpsn.
InterPro; IPR0003006; Ig_MHC.
InterPro; IPR0001; 7tm_1; 1.
Pfam; PF00001; 7tm_1; 1.
PROSITE; PS00237; GPCRHODOPSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS00230; G_PROTEIN_RECEP_F1_2; 1.
PROSITE; PS00230; IG_MHC; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9MZM6 PRELIMINARY;
Q9MZM6;
01-OCT-2000 (TrEMBLrel. 15, C
01-OCT-2000 (TrEMBLrel. 15, L
01-DEC-2001 (TrEMBLrel. 19, L
CHEMOKINE RECEPTOR CXCR4 (FRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Primates.";

Primates.";

Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.

Submitted (JUL-1999) to The EMBL/GenBank/DDBJ databases.

Submitted (JUL-1999) to The EMBL/GenBank/DDBJ databases.
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                                                                                                                                                               6-protein coupled receptor; Glycoprotein; Receptor; Transmembrane NON_TER 1 1 1 1 1 1 1 SEQUENCE 347 AA; 39352 MW; A4FECD8C61FC5AEA CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zheng X.-Z., Zhang Y.-P. "Molecular Evolution of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Callicebus moloch (Dusky titi).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSF
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                                                     Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zhang Y.-P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chordata; Craniata; Vertebrata; Primates; Platyrrhini; Cebidae;
                                                     26.8%;
35.2%;
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34.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ., Geng Z.-C.;
the Chemokine Receptor CXCR4
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Last annotation updat
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Pred. No. 1.96
9; Mismatches
                                                         Score 575.5;
Pred. No. 1.
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Pred. No. 1.9
                                                                                                                                                           A4FECD8C61FC5AEA
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                                             9e-43;
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                                                                                   DB 6;
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                                                                                   Length
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Matches

Conservative

69;

Indels

19;

Gaps

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Qy

Db Db g Qy

g

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Search completed: November 2, 2002, 12:06:56 Job time: 74 secs

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Maximum DB seq length: 2000000000
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/1/paa/VS

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3: /cgn2_6/ptodata/1/paa/VS

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9: /cgn2_6/ptodata/1/paa/VS

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/cgn2_6/ptcodata/1/paa/US099_COMB.pep: *
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Copyright (c) 1993 - 2002 Compugen Ltd.
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                                                                           SUMMARIES
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No.	Score	Query Match	Query Match Length DB	DΒ	ID	Description
1	2142	99.6		اد	1 PCT-US96-00499-2	Sequence 2, Appli
N	2142	99.6	415	_	PCT-US96-00499A-2	Sequence 2, Appli
ω	2142	99.6	415	15	US-09-101-518-2	Sequence 2, Appli
4	2136	99.3	472	-	PCT-US00-26524B-6392	Sequence 6392, Ap
ĸ	1891	87.9	368	15	US-09-170-496-20	Sequence 20, Appl
6	1891	87.9	368	15	US-09-170-496C-20	Sequence 20, Appl
7	1891	87.9	368	15	US-09-170-496D-20	Sequence 20, Appl

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1172.5 901 661 661 637.5 636.5 636.5 635.6	1891 1891 1891 1891 1885 1885 1885 1885
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	-09-624-59 -09-633-54 -09-663-79 -09-170-49 -09-170-49 -09-218-20 -60-213-17 -60-213-17
Sequence 947, App Sequence 255, App Sequence 20, Appl Sequence 20, Appl Sequence 20, Appl Sequence 234, Ap Sequence 1218, Ap Sequence 1218, Ap Sequence 1248, Ap Sequence 1248, Ap Sequence 16, Appl Sequence 66, Appl Sequence 66, Appl Sequence 66, Appl Sequence 66, Appl Sequence 5, Appl Sequence 5, Appl Sequence 741, Appl Sequence 741, Appl Sequence 9, Appl Sequence 9, Appl Sequence 37, Appl Sequence 9, Appl Sequence 4, Appl Sequence 4, Appl	2, AF 2, AF 2, AF 2, AF 174, 174, 174, 174, 424, 424, 424, 424, 424,

ALIGNMENTS

PCT-US96-00499-2 RESULT 1 Sequence 2, Application PC/TUS9600499
GENERAL INFORMATION:
APPLICANT: LI, Yi COUNTRY: USA
ZIP: 07068-1739

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-POS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/00499
FILING DATE:
CLASSIFICATION:
APTORNEY/AGENT INFORMATION:
AMAE: Feiraro, Gregory D
REGISTRATION NUMBER: 36,134
REGISTRATION NUMBER: 36,134
REGISTRATION NUMBER: 36,134 NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS: APPLICANT: LI, YITITLE OF INVENTION: REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 32
TELECOMMUNICATION INFORMATION: ADDRESSEE: Stew.
STREET: 6 Becke.
CITY: Roseland
STATE: NJ ADDRESSEE: E: Carella, Byrne, Bain, Gilfillan, Cecchi,E: Stewart & Olstein6 Becker Farm Road Human G-Protein Chemokine Receptor HSATU68 325800-474

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PCT-US96-00499A-2
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APPLICANT: LI, Yi
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TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                              CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MULLINS, J.G.
                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                               SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
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STREET: 6 Becke
CITY: Roseland
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REGISTRATION NUMBER: 33,073
REFERENCE/DOCKET NUMBER: 32
                                                                                APPLICATION NUMBER: FILING DATE: 11 JA
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Local Similarity 99.8%;
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HSATU68
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     325800-474
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Pred. No. 4.8e-193;
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                                                                                                                                Query Match
Best Local
                                                                                                                                                                                                                                     SEQ ID NO 2
                                                                                                                  Matches
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                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/101,518
CURRENT FILING DATE: 1998-12-21
PRIOR APPLICATION NUMBER: PCT/US96/00499
                                                                                                                                                                                                                                                                                                                                        APPLICANT: Li, Yi
TITLE OF INVENTION:
FILE REFERENCE: PF'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: 201-994-170
TELEFAX: 201-994-174
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 415 amino acid
                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 9 SOFTWARE: Patentin Ver.
                                                                                                                                                                                                                                                                               PRIOR FILING DATE:
                                                                                                                                                                                        TYPE: PRT
ORGANISM: Homo
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                                                                                                                                Local Similarity
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             AEVAALLENFSSSYDYGENESDSCCTSPPCPQDFSLNFDRAFLPALYSLLFLLGLLGNGA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MRLVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVTSGLGYMHCCL
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                                                                       MELRKYGPGRLAGTVIGGAAQSKSQTKSDSITKEFLPGLYTAPSSPFPPPSQVSDHQVLND
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AEVAALLENFSSSYDYGENESDSCCTSPPCPQDFSLNFDRAFLPALNSLLFLLGLLGNGA
                                                        MELRKYGPGRLAGTVIGGAAQSKSQTKSDSITKEFLPGLYTAPSSPFPPSQVSDHQVLND 60
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                                                                                                                 Score 2142; DB 15;
Pred. No. 4.8e-193;
0; Mismatches 1;
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Pred. No. 4.8e-193;
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; LENGTH: 472
; TYPE: PRT
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Best Local S
Matches 413
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GENERAL INFORMATION:
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TITLE OF INVENTION: COLOn and Colon Cancer Associated
FILE REFERENCE: PA005PCT
CURRENT APPLICATION NUMBER: PCT/US00/26524B
CURRENT FILING DATE: 2000-99-28
PRIOR APPLICATION NUMBER: 60/157,137
PRIOR FILING DATE: 1999-09-29
PRIOR FILING DATE: 1999-09-29
PRIOR FILING DATE: 1999-11-03
NUMBER: OF SEQ. ID NOS: 8564
                                                                                                                                                                                                                                          PEATURE:
NAME/KEY: SITE
LOCATION: (139)
OTHER INFORMATION: Xaa e
NAME/KEY: SITE
LOCATION: (164)
OTHER INFORMATION: Xaa e
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nes 413; Conserv
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99.5%;
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Pred. No. 2.1e-192;
0; Mismatches 2;
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Sequence 20, Application US/09170496C GENERAL INFORMATION:
APPLICANT: Behan, Dominic P.
APPLICANT: Chalmers, Derek T.
APPLICANT: Liaw, Chen W.
TITLE OF INVENTION: Non-Endogenous, Co
TITLE OF INVENTION: Receptors
FILE REFERENCE: AREN-0040
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LENGTH: 368
TYPE: PRT
ORGANISM: Homo sapiens
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US-09-170-496C-20
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US-09-170-496-20
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Best Local S
Matches 364
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nes 364; Conserv
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Sequence 20, Application US/09170496 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/170,496
CURRENT FILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 286
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                                                                                                         VSRGQRRLRAMRLVVVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVT
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                      SGLGYMHCCLNPLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSSWSETSEA 410
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SGLGYMHCCLNPLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSSWSETSEA
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Pred. No. 2.1e-169;
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Constitutively Activated Human G Protein-Coupl

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; SEQ ID NO 20
; LENGTH: 368
; TYPE: PRT
; ORCANISM: Homo sapiens
US-09-170-496D-20
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CURRENT FILTMG DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 286
SOFTWARE: Patentin version 3.0
SEQ ID NO 20
LENGTH: 368
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                             Matches
                                                                                                                       Query Match
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APPLICANT: Chalmers, Derek T.
APPLICANT: Liaw, Chen W.
TITLE OF INVENTION: Non-Endogenous, Constitutively Activated Human G Protein-Coupled TITLE OF INVENTION: Receptors
FILE REFERENCE: ARRN-0040
                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/170,496D
CURRENT FILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 294
SOFTWARE: Patentin version 3.1
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Local Similarity 99.7%;
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                                                                                                        87.9%;
99.7%;
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Pred. No. 2.1e-169;
1; Mismatches 0;
                                                                                          Score 1891; DB 15;
Pred. No. 2.1e-169;
1; Mismatches 0;
                                                                                                                    Length
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                                                                 Best Loc
Matches
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GENERAL INFORMATION:
APPLICANT: Loctscher, Marce
APPLICANT: Moser, Bernhard
                                                                                               Query Match
                                                                                                                                                                                                                                      TELEFAX: (617) 861-95. INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/09/624,594
FILING DATE: 25-JUL-2000
PRIOR APPLICATION UNMBER: US/08/709,838
FILING DATE: 10-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 368 amino acid
                                                                                                                                                                                                                                                                     TELEPHONE: (617) 861-6240
                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Brook Esq., David
REGISTRATION NUMBER: 22,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: IP-10/MIG RECEPTOR DESIGNATED CXCR3, TITLE OF INVENTION: NUCLEIC ACIDS, AND METHODS OF USES THE NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                184
                                                                                                                                                             TYPE: amino acid
TOPOLOGY: linear
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ZIP: 02173
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                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: TKI96-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Lexington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Hamilton, Brook
STREET: Two Militia Drive
                                                                                 Local
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                 QVSDHQVLNDAEVAALLENFSSSYDYGENESDSCCTSPPCPQDFSLNFDRAFLPALYSLL 110
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EVSDHQVLNDAEVAALLENFSSSYDYGENESDSCCTSPPCPQDFSLNFDRAFLPALYSLL 63
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                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Application US/09624594
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                                                                                                                                                                                                368 amino acids
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                                                                 Conservative
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IBM PC compatible
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                                                                               87.9%;
99.7%;
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                                                                                                                                                                                                                                                                                                                       22,592
                                                             Score 1891; DB 20; Pred. No. 2.1e-169; 1; Mismatches 0;
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                                                                                               Length
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US-09-633-541-2
; Sequence 2, Application US/09633541
; GENERAL INFORMATION:
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                                                                                                      US-09-633-541-2
                             Query Match
Best Local Similarity
Matches 364; Conserv
                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Brook Esq., David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: TKI9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
                                                                                                                                                                                INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Loetscher, Marcel APPLICANT: Moser, Bernhard
                                                                                                                  MOLECULE TYPE: protein
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                                                                                                                              LENGTH: 368 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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51 QVSDHQVLNDAEVAALLENFSSSYDYGENESDSCCTSPPCPQDFSLNFDRAFLPALYSLL 110
                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
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                                  Conservative
                                                  87.9%;
99.7%;
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                                                                                                                                                                                                                                                                                                                                                       08/709,838
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                             Score 1891; DB 20; Length 368;
Pred. No. 2.1e-169;
1; Mismatches 0; Indels 0
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                               Gaps
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TOPOLOGY: linear;

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SUS-09-663-702-2
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                                                                                                                     REFERENCE/DOCKET NUMBER: 7
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     364
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                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/663,702
FILING DATE: 15-Sep-2000
CLASSIFICATION: CUnknown>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook
STREET: Two Militia Drive
                                                                                                                                                                                                                                      APPLICATION NUMBER: 08/829,839 FILING DATE: <Unknown> ATTORNEY/AGENT INFORMATION:
                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VSRGQRRLRAMRLVVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVT 350
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                                                                       LENGTH: 368 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Lexington STATE: MA
                                                                                                                                                                                                       NAME: Brook Esq., David E. REGISTRATION NUMBER: 22,592
                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: U
ZIP: 02173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mackay, Charles R.
OF INVENTION: IP-10/MIG RECEPTOR DESIGNATED CXCR3
ANTIBODIES, NUCLEIC ACIDS, AND METH
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                      NO:
                                                                                                                                                                                         TKI96-01A
                      <u>ب</u>
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                                                                                                                                                                                                                                                                                                                                                                          Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             METHODS OF USE THEREFOR
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US-09-663-799-2
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Best Local
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                                    INFORMATION FOR SEQ ID NO:
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                                                           APPLICATION NUMBER: 08/709,838
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Brook Esq., David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: TK196-01
TELEPHONE: (617) 861-6240
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                                                                                                                                                                                                                                                                                                                   ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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ADDRESSEE: Hamilton, Brook,
STREET: Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Moser, Bernhard
TITLE OF INVENTION: IP-10/MIG RECEPTOR DESIGNATED CXCR3,
NUCLEIC ACIDS, AND METHODS OF USES T
                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Loetscher, Marcel
                                                                                                                                                                                              PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 4
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                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                         APPLICATION NUMBER: US/09/663,799
FILING DATE: 15-Sep-2000
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                       CITY: Lexington STATE: MA
                                                 TELEFAX:
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   LENGTH:
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368 amino acids
                                                   (617) 861-9540
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Pred. No. 2.1e-169;
1; Mismatches 0;
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TOPOLOGY: linear;
MOLECULE TYPE: protein;
SEQUENCE DESCRIPTION: SEQUS-09-663-799-2
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US-09-170-496C-174
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SOFTWARE: PatentIn version 3.0
SEQ ID NO 174
LENGTH: 368
TYPE: nom
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Behan, Dominic P. APPLICANT: Chalmers, Derek T. APPLICANT: Liaw, Chen W.
                                                                           111 FLLGLLGNGAVAAVLLSRRTALSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGL 170
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                                                                                                                      EVSDHQVLNDAEVAALLENFSSSYDYGENESDSCCTSPPCPQDFSLNFDRAFLPALYSLL
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CKVAGALENINFYAGALLLACISFDRYLNIVHATQLYRRGPPARVTLTCLAVWGLCLLFA
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99.78;
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Pred. No. 2.1e-169;
1; Mismatches 0;
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APPLICANT: Llaw, Chen W.
TITLE OF INVENTION: Non-Endogenous, Constitut
TITLE OF INVENTION: Receptors
FILE REFERENCE: AREN-0040
CURRENT APPLICATION NUMBER: US/09/170,496D
CURRENT APPLICATION NUMBER: 1998-10-13
NUMBER OF SEQ ID NOS: 294
SOFTWARE: PatentIn version 3.1
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    RESULT 14
US-09-010-701C-22
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LENGTH: 368
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Local Similarity 99.5%;
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|SRGQRRLRAKRLVVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVT
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                                                                                                                  SGLGYMHCCLNPLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSSWSETSEA
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Pred. No. 7.7e-169;
1; Mismatches 1;
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Matches
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APPLICATION UMBER: US/09/010,701C
FILING DATE: 22-JAN-1998
CLASSIFICATION:
PRIOR APPLICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 22, Application US/09010701C GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
COMPUTER TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (650)496-1200 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:

NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX06
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650)852-9196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 367 amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
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                             303
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                                                                                                                                                                                                                                                            63
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 901 Cali
                                                                                                                                                                                                                                                                                                                                            51 QVSDHQVLNDAEVAALLENFSSSYDYGENESDSCCTSPPCPQDFSLNFDRAFLPALYSLL 110
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SYSGL 415
                                                                                                                                        FLLGLLGNGAVAAVLLSQRTALSSTDTFLLHLAVADVLLVLTLPLWAVDAAVQWVFGPGL
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                            SGMGYMHCCLNPLLYAFVGVKFREKMWMLFTRLGRSDQRGPQRQPSSSRRESSWSETTEA
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Hedrick, Joseph A.
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86.0%; Pred. No. 2e-144;
Live 22; Mismatches 28;
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Gaps

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122

362

302 350 242 290

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Sequence 107, Application US/60258273

SEQUENCE 107, Application US/60258273

GENERAL INFORMATION:

APPLICANT: Beasley, Ellen

TITLE OF INVENTION: ISOLATED HUMAN NUCLEAR HORMONE RECEPTOR

TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN NUCLEAR

TITLE OF INVENTION: HORMONE RECEPTOR PROTEINS, AND USES THEREOF

FILE REFERENCE: CL001042-PROV

CURRENT APPLICATION NUMBER: US/60/258,273

CURRENT FILING DATE: 2000-12-27

NUMBER OF SEQ ID NOS: 312

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 107

LENGTH: 380

TYPE: PRT

ORGANISM: Human

US-60-258-273-107
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US-60-258-273-107
Search completed: November Job time: 203 secs
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                                                                                                                           AVDAAVQWVFGSGLCKVAGALENINFYAGALLLACISFDRYLNIVHATQLYRRGPPARVT 216
                                                                               CGRESRVDVAKSVTSGLGYMHCCLNPLL 364
                                                                                                                                                                                                                                                                                                                                            NFDRAFLPALYSLLFLLGLLGNGAVAAVLLSRRTALSSTDTFLLHLAVADTLLVLTLPLW 156
                                                                                                                                                                                                                                                                                                                                                                                        TPPSSQSTSPAMVLEVSDHQVLNDAEVAALLENFSSSYDYGENESDSCCTSPPCPQDFSL 71
                                                             CGRESRV-----VRGQVGHLRPGLHALL
                                                                                                                                                                                                                                                                                                                            NFDRAFLPALYSLLFLLGLLGNGAVAAVLLSRRTALSSTDTFLLHLAVADTLLVLTLPLW 131
             2,
               2002, 12:14:54
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GenCore version 5.1.3

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us-09-101-518a-2 Fapn
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protein - pro	ght (c) 1993 - 2002 Compugen Ltd. rch, using sw model	
Run on:	November 2, 2002, 12:07:05; Search time 123 Seconds (without alignments) 1014.235 Million cell updates/sec	
Title: U Perfect score: 2 Sequence: 1	US-09-101-518A-2 2151 1 MELRKYGPGRLAGTVIGGAAsssrrdsswsetseasysgl 415	
Scoring table: E	BLOSUM62 Gapop 10.0 , Gapext 0.5	
Searched: 1	1112697 seqs, 300604653 residues	
Total number of h	hits satisfying chosen parameters: 1112697	
Minimum DB seq le Maximum DB seq le	length: 0 length: 2000000000	
Post-processing:	Minimum Match 0% Maximum Match 100% Listing first 45 summaries	
Database :	Pending_Patents_AA_New:* 1: /cgn2_6/ptodata/2/paa/PCT_NEW_COMB.pep:* 2: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep:* 3: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep:* 4: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep:* 5: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep:* 6: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:* 7: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:* 8: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:* 9: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:* 10: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:* 11: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep:* 12: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep:* 13: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep:* 14: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep:* 15: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pep:*	
Pred. No. i score great and is deri	is the number of results predicted by chance to have a ster than or equal to the score of the result being printed, ived by analysis of the total score distribution.	
ore	SUMMARIES ery tch Length DB ID Description	
1 2151 2 2136 2 2136 3 1891 4 1891 5 1885 6 61 7 661 7 661 8 633 110 633 111 633 112 633 113 633 114 606.5 610 15 606.5 16 606.5	415 9 US-09-101-518A-2 368 11 US-10-106-698-6402 Sequent 368 11 US-10-251-385-20 Sequent 368 11 US-10-251-385-20 Sequent 368 11 US-10-251-385-20 Sequent 369 11 US-10-251-385-20 Sequent 370 11 US-10-251-385-66 Sequent 377 11 US-10-251-385-66 Sequent 372 11 US-10-251-385-66 Sequent 372 11 US-10-251-385-66 Sequent 372 11 US-10-251-385-9 Sequent 378 11 US-10-251-385-200 Sequent 370 11 US-10-251-385-200 Sequent 370 11 US-10-251-385-200 Sequent 370 11 US-10-105-105-105-105-105-105-105-105-105-	
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566	566.5	567.5	567.5	570.5	576.5	576.5	576.5	576.5	576.5	576.5	576.5	577.5	584	584	586	586	586	588	602	602	602	602	602	602
26.3	26.3	26.4	26.4	26.5	26.8	26.8	26.8	26.8	26.8	26.8	26.8	26.8	27.2	27.2	27.2	27.2	27.2	27.3	28.0	28.0	28.0	28.0	28.0	28.0
378	378	378	378	353	352	352	352	352	352	352	352	352	378	359	378	378	378	399	378	378	378	378	378	378
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US-09-686-020A-7	US-10-164-649-5	US-10-224-855-16	US-09-694-401A-16	US-10-143-982-200	US-10-014-322A-126	US-10-160-401-3	US-10-151-274-4	US-09-647-501-2	US-09-646-785A-1	US-09-813-651B-85	PCT-US01-51165-126	US-09-625-573-6	US-10-251-385-204	US-09-646-785A-3	US-10-251-385-74	US-10-224-855-13	US-09-694-401A-13	US-10-143-982-244	US-10-219-917-240	US-10-216-893-220	US-10-216-436-526	US-10-216-428-142	US-10-213-073-338	US-10-212-054-862
Sequence 7, Appli	Sequence 5, Appli	Sequence 16, Appl	Sequence 16, Appl	Sequence 200, App	Sequence 126, App	Sequence 3, Appli	Sequence 4, Appli	Sequence 2, Appli	Sequence 1, Appli		Sequence 126, App	Sequence 6, Appli	Sequence 204, App	Sequence 3, Appli	Sequence 74, Appl	Sequence 13, Appl	Sequence 13, Appl	`	Sequence 240, App	•	526,	Sequence 142, App	Sequence 338, App	-

ALIGNMENTS

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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-101-518A-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 1
US-09-101-518A-2
                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Human G-Protein Chemokine Receptor HSATU68
FILE REFERENCE: PF218US
CURRENT APPLICATION NUMBER: US/09/101,518A
CURRENT APPLICATION NUMBER: US/09/101,518A
CURRENT FILING DATE: 2002-03-18
PRIOR APPLICATION NUMBER: PCT/US96/00499
PRIOR FILING DATE: 1996-01-11
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin version 3.1
SEQ ID NO 2
                                                                                                                                                                                                                                                                                    Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 415; Conservative C
             241 HDERLNATHCQYNFPQVGRTALRVLQLVAGFLLPLLVMAYCYAHILAVLLVSRGQRRLRA 300
                                                                                   181
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HDERLNATHCQYNFPQVGRTALRVLQLVAGFLLPLLVMAYCYAHILAVLLVSRGQRRLRA
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Pred. No. 6.1e-174;
D; Mismatches 0;
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LENGTH: 472
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PRIOR ETLING DATE: 2000-09-28
PRIOR EPLICATION NUMBER: US 60/157,137
PRIOR FILING DATE: 199-09-29
PRIOR APPLICATION NUMBER: US 60/163,280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/10/106,698 CURRENT FILING DATE: 2002-03-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide FILE REFERENCE: PA005P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE: 1999-11-03
NUMBER OF SEQ ID NOS: 8564
SOFTWARE: Patentin Ver. 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Ruben et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: MISC_FEATURE
LOCATION: (139)
OTHER INFORMATION: Xaa equals any
NAME/KEY: MISC_FEATURE
LOCATION: (164)
OTHER INFORMATION: Xaa equals any
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ORGANISM: Homo sapiens
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MELRKYGPGRLAGTVIGGAAQSKSQTKSDSITKEFLPGLYTAPSSPFPPSQVSDHQVLND 60
                                                     NPLLYAFYGYKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSSWSETSEASYSGL 415
                                                                                                                                                                                                                                                                                                                                                                                                                                     AEVAALLENFSSSYDYGENESDSCCTSPPCPQDFSLNFDRAFLPALYSLLFLLGLLGNGA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NPLLYAFYGYKFRERWWMLLLRLGCPNQRGLQRQPSSSRRDSSWSETSEASYSGL 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MRLVVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVTSGLGYMHCCL 360
                                                                                                                                                                                                                                                               NFYAGALLLACISFDRYLNIVHATQLYRRGPPARVTLTCLAVWGLCLLFALPDFIFLSAH 240
                                                                                                                                                                                               HDERLNATHCQYNFPQVGRTALRVLQLVAGFLLPLLVMAYCYAHILAVLLVSRGQRRLRA
                                                                                                                                                                                                             HDERLNATHCQYNFPQVGRTALRVLQLVAGFLLPLLVMAYCYAHILAVLLVSRGQRRLRA 300
                                                                                                                                                                                                                                                                                                                                                                                                       AEVAALLENFSSSYDYGENESXSCCTSPPCPQDFSLNFDRAFLPALXSLLFLLGLLGNGA 177
                                                                                                                                                                                                                                                                                                                                    VAAVLLSRRTALSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGLCKVAGALFNI 237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99.3%;
99.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 2136; DB 11;
Pred. No. 1.3e-172;
0; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of the naturally occurring L-amino
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                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (617) 861-62.
TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 2:
                   351
                                                                                                                         184
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APPLICATION NUMBER: US/10/251,686
FILING DATE: 20-Sep-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: IP-10/MIG RECEPTOR DESIGNATED CXCR3,
ANTIBODIES, NUCLEIC ACIDS, AND METHODS OF USE THEREFOR
                                                                     VSRGQRRLRAMRLVVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVT 350
                                                                                                                                                                                                             CKVAGALFNINFYAGALLLACISFDRYLNIVHATQLYRRGPPARVTLTCLAVWGLCLLFA 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Loetscher, Marcel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
SGLGYMHCCLNPLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSSWSETSEA 410
                                                                                                                                         LPDF1FLSAHHDERLNATHCQYNFPQVGRTALRVLQLVAGF1LLPLLVMAYCYAH1LAVLL
                                                                                                                                                                                           CKVAGALFNINFYAGALLLACISFDRYLNIVHATQLYRRGPPARVTLTCLAVWGLCLLFA 183
                                                                                                                                                                                                                                                                               FLLGLLGNGAVAAVLLSRRTALSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGL 170
                                                     VSRGQRRLRAMRLVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVT
                                                                                                                       LPDFIFLSAHHDERLNATHCQYNFPQVGRTALRVLQLVAGFLLPLLVMAYCYAHILAVLL
                                                                                                                                                                                                                                                             FLLGLLGNGAVAAVLLSRRTALSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGL 123
                                                                                                                                                                                                                                                                                                                                                                                                     364;
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CITY: Lexington
STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/829,839
FILING DATE: 31-MAR-1997
APPLICATION NUMBER: US 08/709,838
FILING DATE: 10-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: TKI96-01A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Brook Esq., David E. REGISTRATION NUMBER: 22,592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Hamilton,
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99.78;
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Pred. No. 5.8e-152;
1; Mismatches 0;
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US-10-251-385-174
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US-10-251-385-20
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                                                                                                     Sequence 174, Application US/10251385 GENERAL INFORMATION:
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LENGTH: 368
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Best Local Similarity 99.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
APPLICANT: Behan, Dominic P.
APPLICANT: Chalmers, Derek T.
APPLICANT: Liaw, Chen W.
TITLE OF INVENTION: Non-Endogenous, Constitutively Activated Human
TITLE OF INVENTION: Protein-Coupled
TITLE OF INVENTION: Receptors
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Pred. No. 5.8e-152;
1; Mismatches 0;
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; ORGANISM: Homo
US-10-251-385-174
                                                                                                                                                   PRIOR FILING DATE: 1998-04-16
NUMBER OF SEQ ID NOS: 32
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 20
LENGTH: 357
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                              Sequence 20, Application US/09694401A
GENERAL INFORMATION:
APPLICANT: GONZAIO, Jose Angel
APPLICANT: Gutierrez-Ramos, Jose Ca
 Query Match
Best Local Similarity
Matches 141; Conserv
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Best Local :
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SOFTWARE: Patentin version 3.1
SEQ ID NO 174
LENGTH: 368
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                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/694,401A CURRENT FILING DATE: 2000-10-23 PRIOR APPLICATION NUMBER: US 09/294,058 PRIOR FILING DATE: 1999-04-16 PRIOR APPLICATION NUMBER: US 09/061,753
                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Gutierrez-Ramos, Jose Carlos
TITLE OF INVENTION: NOVEL MOLECULES OF THE BGCKR-RELATED PROTEIN FAMILY AND USES
FILE REFERENCE: 07334-317001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: AREN-0040
CURRENT APPLICATION NUMBER: US/10/251,385
CURRENT FILING DATE: 2002-09-20
PRIOR APPLICATION NUMBER: US/09/170,496
PRIOR FILING DATE: 1998-10-13
                                                                                     FEATURE:
OTHER INFORMATION:
                                                                                                                            ORGANISM: Artificial Sequence
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                                                                                           Consensus
                   30.7%;
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99.5%;
; Score 661; DB 9;
; Pred. No. 1e-47;
65; Mismatches 122
                                                                                           sequence
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Pred. No. 1.9e-151;
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                                  Length 357;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 20
LENGTH: 357
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 20, Application US/10224855
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                   Query Match 30.7%; Score 661; DB 11; Best Local Similarity 40.1%; Pred. No. 1e-47; Matches 141; Conservative 65; Mismatches 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/10/224,855
CURRENT FILING DATE: 2002-08-21
PRIOR APPLICATION NUMBER: US/09/694,401
PRIOR FILING DATE: 2000-10-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR FILING DATE: 1998-04-16
NUMBER OF SEQ ID NOS: 32
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 09/294,058
PRIOR FILING DATE: 1999-04-16
PRIOR APPLICATION NUMBER: US 09/061,753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Gutierrez-Ramos, Jose Carlos
TITLE OF INVENTION: NOVEL MOLECULES OF TI
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 07334-317001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Gonzalo, Jose Angel APPLICANT: Gutierrez-Ramos, J
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181
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LSGDVRCSPIYPSSEGTALKALIQGLEMVIGFFVPLLAMAFCYLIIIKTLLQAQNSKRHK 240
                                   RLNATHCQYNFPQVGRTALRV----LQLVAGFLLPLLVMAYCYAHILAVLLVSRGQRRLR 299
                                                                                                  LLACISFDRYLNIVHATQLYRRGPPARVTL----TCLAVWGLCLLFALPDFIFLSAHHDE 243
                                                                                                                                                        YKKLRTMTDVYLLNLAVADLLELLTLPFWAVSAAHGWVFGVAMCKLLSGIYTVNFVSGML 124
                                                                                                                                                                                                                                        ENTTSYVDYSQYEL-----LCSKEDVRNFAKVFLPIMYSLIFVVGLLGNSLVVLTYAY 64
                                                                                                                                                                                                                                                                             ENFSSSYDYGENESDSCCTSPPCPQDFSLNFDRAFLPALYSLLFLLGLLGNGAVAAVLLS 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LNPLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSSWSETSEAS 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RLNATHCQYNFPQVGRTALRV----LQLVAGFLLPLLVMAYCYAHILAVLLVSRGQRRLR 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LLACISFDRYLNIVHATQLYRRGPPARVTL----TCLAVWGLCLLFALPDFIFLSAHHDE 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YKKLRTMTDVYLLNLAVADLLFLLTLPFWAVSAAHGWVFGVAMCKLLSGIYTVNFVSGML 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ENTTSYVDYSQYEL-----LCSKEDVRNFAKVFLPIMYSLIFVVGLLGNSLVVLTYAY
                                                                       RRTALSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGLCKVAGALFNINFYAGAL 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LNPVLYAFIGVKFRNYLMKLAKDLGC-----LRREQWSSARHRESSISREFS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LLACISIDRYIAIVQATSAHRH--RSRVLLISKVICVGVWVLAILLSIPELVFSTV--NE 180
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                                                                                                                                                                                                                                                                                                                                                        DB_11; Length 357;
                                                                                                                                                                                                                                                                                                                       Indels
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                                                                                                                     US-09-101-518A-9
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Sequence 9, Application US/09101518A
GENERAL INFORMATION:
APPLICANT: Li, Vi
TITLE OF INVENTION: Human G-Protein Chemokine Receptor HSATU68
FILE REFERENCE: PF218US
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LENGTH: 372
TYPE: PRT
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GENERAL INFORMATION:
APPLICANT: Behan, Dominic P.
APPLICANT: Chalmers, Derek T.
APPLICANT: Liaw, Chen W.
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Best Local !
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CURRENT FILING DATE: 2002-09-20
PRIOR APPLICATION NUMBER: US/09/170,496
PRIOR FILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 294
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TITLE OF INVENTION: Protein-Coupled
TITLE OF INVENTION: Receptors
FILE REFERENCE: AREN-0040
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                                                                                                                                                                                                                                                                                                              249 QRRPQRQKAVRVAILVTSIFFLCWSPYHIVIFLDTLARLKAVDNTCKLNGSLPVAITMCE 308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29.5%; Score 635; DB 11; Local Similarity 40.8%; Pred. No. 1.7e-45; les 147; Conservative 50; Mismatches 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENLEDLFWELDRLDNYNDTSLVENHLCPATEGPLMASFKAVFVPVAYSLIFLLGVIGNV 70
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                                                                                                                                                                                                                     FLGLAHCCLNPMLYTFAGVKFRSDLSRLLTKLGCTGPASLCQLFPSWRR-SSLSESENAT
                                                                                                                                                                                                                                                                                                                                                                                                           SQGHHNNSL--PRCTFSQENQAETHAWFTSRFLYHVAGFLLPMLVMGWCYVGVVHRLRQA 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LVLVILERHRQTRSSTETFLFHLAVADLLLVFILPFAVAEGSVGWVLGTFLCKTVIALHK 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LNPVLYAFIGVKFRNYLMKLAKDLGC----LRREQWSSARHRESSISREFS
                                                                                                                                                                                                                                                                                                                                                          SRGQRRLRAMRLVVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                     -SAHHDERLNATHCQYNFPQVGRT----ALRVLQLVAGFLLPLLVMAYCYAHILAVL-LV 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFYAGALLLACISFDRYLNIVHATQLYRRGPPARVTLTCLAVWGLCLLFALPDFIFL-- 237
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CURRENT APPLICATION NUMBER: US/09/101,518A CURRENT FILING DATE: 2002-03-18 PRIOR APPLICATION NUMBER: PCT/US96/00499 PRIOR FILING DATE: 1996-01-11

NUMBER OF

SEQ ID NOS:

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US-09-625-573-8
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TYPE: PRT
ORGANISM: Homo sapiens
     INFORMATION FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               134
                                                                                                                                                                                  COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS_MS-DOS
SOFTWARE: PATENTIN Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/09/625,573
FILING DATE: 25-Jul-2000
CLASSIFICATION: CURROWN>
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               74
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                                                                                                                                  APPLICATION NUMBER: US/08/446,669 FILING DATE: May 25, 1995 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Coughlin, Shaun
TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
PROTEIN RECEPTORS
                                                                   TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Charo,
                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SNVSPA-C---YEDMGNNTANWRMLLRILPQSFGFIVPLLIMLFCYGFTLRTLFKAHMGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSCLNPLIYAFIGQKFRHGLLKILAIHGLISKDSLPKDSRPSFVGSSSGHTS 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KHRAMRVIFAVVLIFLLCWLPYNLVLLADTLMRTQVIQETCERRNHIDRALDATEILGIL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RSVTDVYLLNLALADLLFALTLPIWAASKVNGWIFGTFLCKVVSLLKEVNFYSGILLLAC 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HCCLNPLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSSWSETS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RLRAMRLVVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVTSGLGYM 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ISFDRYLNIVHATQLYRRGPPARVTLT------CLAVWGLCLLFALPDFIFLSAHHD 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ISVDRYLAIVHATR-----TLTQKRYLVKFICLSIWGLSLLLALPVLLFRRTVYS 183
                                                                              NAME: Neeley, Richard
REGISTRATION NUMBER: 30,092
REFERENCE/DOCKET NUMBER: UC
TELEFAX: 415-857-0663
TELEX: 380816CooleyPA
DN FOR SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                     CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                       ZIP: 94306-2155
                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 5 Palo Alto Square
                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Cooley Godward Castro Huddleson
                                                  TELEPHONE: 415-843-5000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   version
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                                                                                   UCAL-237/01US
                                                                                                                                                                                                                                                                    Version #1.25
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; ORGANISM: Homo PCT-US02-07946A-16
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PCT-US02-07946A-16
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                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn SEQ ID NO 16 LENGTH: 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 16, Application PC/TUS0207946A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                         Matches 141;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Theodore Torphy
TITLE OF INVENTION: CHRONIC OBSTRUCTIVE PULMONARY DISEASE-RELATED
TITLE OF INVENTION: IMMUNOGLOBULIN
TITLE OF INVENTION: DERIVED PROTEINS, COMPOSITIONS, METHODS AND COMPOSITION OF THE REFERENCE: CEN-0286 PCT CURRENT APPLICATION NUMBER: PCT/US02/07946A
CURRENT FILING DATE: 2002-03-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
       140
                           192 ISFDRYLNIVHATQLYRRGPPARVTLT-------CLAVWGLCLLFALPDFIFLSAHHD 242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                             LSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGLCKVAGALFNINFYAGALLLAC 191
                                                                                                                                                                                           SNYSYSSTLPPFLLDAAPCEPE-SLEINKYFVVIIYALVFLLSLLGNSLVMLVILYSRVG 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HCCLNPLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSSWSETS 408
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ISFDRYLNIVHATQLYRRGPPARVTLT------CLAVWGLCLLFALPDFIFLSAHHD 242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ISVDRYLAIVHATR------TLTQKRYLVKFICLSIWGLSLLLALPVLLFRRTVYS 184
                                                                                                RSVTDVYLLNLALADLLFALTLPIWAASKVNGWIFGTFLCKVVSLLKEVNFYSGILLLAC
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                                                                                                                                                                                                                                                                                    29.4%; Score 633; DB 2; 40.1%; Pred. No. 2.4e-45; vative 51; Mismatches 130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DERIVED PROTEINS, COMPOSITIONS, METHODS AND USES
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-TLTQKRYLVKFICLSIWGLSLLLALPVLLFRRTVYS 189
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RESULT 13
US-10-251-385-200
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US-10-099-007A-16
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CURRENT FILTMG DATE: 2002-03-14
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver 2.0
SEQ ID NO 16
                                                                                                                                                                                  Sequence 200, Application US/10251385 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 16, Application US/10099007A GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local
TITLE OF INVENTION: Non-Endogenous, Const.
TITLE OF INVENTION: Protein-Coupled
TITLE OF INVENTION: Receptors
FILE REFERENCE: AREN-0040
CURRENT APPLICATION NUMBER: US/10/251,385
CURRENT FILING DATE: 2002-09-20
                                                                                                                       APPLICANT: Chalmers, Der APPLICANT: Liaw, Chen W.
                                                                                                                                          APPLICANT: Behan, Dominic P. APPLICANT: Chalmers, Derek T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: CHRONIC OBSTRUCTIVE PULOMARY DISEASE-RELATED IMMUNOGLOBULIN TITLE OF INVENTION: DERIVED PROTEINS, COMPOSITIONS, METHODS AND USES FILE REFERENCE: CEN-0286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Theodore Torphy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 360
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                            306
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                                                                                                                                                                                                                                                                                                                                             HCCLNPLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSSWSETS 408
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                                                                                                                                                                                                                                                                                                                                                                                     KHRAMRVIFAVVLIFLLCWLPYNLVLLADTLMRTQVIQETCERRNHIDRALDATEILGIL
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40.1%; Pred. No. 2.4e-45;
ative 51; Mismatches 130
                                                                                                  Constitutively Activated
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Matches
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SEQ ID NO 194
LENGTH: 377
                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 194 Application US/10143982
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PTZ38CIM
CURRENT APPLICATION NUMBER: US/10/143,982
CURRENT FILING DATE: 2002-05-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US/09/170,496
PRIOR FILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 294
SOFTWARE: PatentIn version 3.1
SEQ ID NO 200
LENGTH: 372
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                                                                                                                                                                                                                                              Query Match
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                  ETEEDMSNITDPQMWDFDDLNFTGMPPADEDYSPCMLETETLNKYVVIIAYALVFLLSLL
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 LKEVNFYSGILLLACISVDRYLAIVHATR--
                                                                 GNSLVMLVILYSRVGRSVTDVYLLNLALADLLFALTLPIWAASKVNGWIFGTFLCKVVSL 142
                                                                                                   GNGAVAAVLLSRRTALSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGLCKVAGA 176
                                                                                                                                                                       ENESDSCCTSPPCPQDF-SLNF-----DRAFLPAL------YSLLFLLGLL 116
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                                                                                                                                                                                                        28.4%; Score 610; DB 11; 38.9%; Pred. No. 2.3e-43; tive 48; Mismatches 129
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Sequence 3, Application PC/TUS0215638

GENERAL INFORMATION:
APPLICANT: Genalssance Pharmaceuticals, Inc.
APPLICANT: Bieglacki, Karyn M.
APPLICANT: Denton, R. Rex
APPLICANT: Lee, Helen H.
APPLICANT: Nandabalan, Krishnan
TITLE OF INVENTION: HAPPLOTYPES OF THE ILBRA GENE
FILE REFERENCE: WMH-0441PCT
CURRENT APPLICATION NUMBER: PCT/US02/15638
CURRENT APPLICATION NUMBER: 60/291,533
PRIOR APPLICATION NUMBER: 60/291,533
PRIOR APPLICATION NUMBER: 50/291,533
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Search completed: November Job time : 126 secs
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                                                                                                                        GONFRHGFLKILAMHGLVSKEFLARHRVTSYTSSSVNVSS 348
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Title:
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Sequence:
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-MODEL-frame+_p2n.model -DEV=xlh
-Q-/cgn2_1/USPTO_spool/US09101518/runat_29102002_091101_24/app_query.fasta_1.583
-Q-/cgn2_1/USPTO_spool/US09101518/runat_29102002_091101_24/app_query.fasta_1.583
-DB-GenEmb1 -QFWF-fastap -SUFFIX-P2n.rge -MINMATCH-0.1 -LOOPCL-0 -LOOPEXT-0
-UNITS-bits -START-1 -END--1 -MATRIX-biosum62 -TRANS-human40.cdi -LIST-45
-DOCALIGN-200 -THR_SCORE-pct -THR_MAX-100 -THR_MIN-0 -ALIGN-15 -MODE-LOCAL
-OUTFMT-pto -NORM-ext -HEAPSIZE-500 -THR_MILEN-0 -MAXLEN-200000000
-USER-US09101518 @CGN_1 _1182 @runat_29102002_091101_24 -NCPU-6 -ICPU-3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES-0 -WAIT -LONGLOG -DEV_TIMEOUT-120
-WARN_TIMEOUT-30 -THREADS-1 -XGAPOP-10 -XGAPEXT-0.5 -FGAPOP-6 -FGAPEXT-7
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Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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em_htg_hum:*
em_htg_inv:*
em_htg_other:*
em_htgo_inv:*
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Pred. No. score grea d. No. is the number of results predicted by chance to have a re greater than or equal to the score of the result being printed, is derived by analysis of the total score distribution.

SUMMARIES

Result ö Score Query Match Length 262652 1236 271144 1060 1122 1068 1232 1206 1206 . 2245 . 4452 9269 98433 1060 1060 3011 1670 1678 1525 BB 10 6 909 စ စ O NRGPCNLR AR107998 O MMBLR1 HUMIL8RB 1 G28560 HSIL8RB4 HUMIL8R HUMILBR HSBLRIA HSMDCR AP000909 E11245 AP000877 AP000877 AP0002357 MMMCILBRB AX281745 PTILBRB MMILBRA RABILBC RABILBC RABILBC HUMIL8RAB AC097483 GGIL8RB 124456 113755 HUMILEU8R AR107999 AR151870 AR117009 HSGPCRIN8 AF223642 AB003174 AF045146 AC105645 AR015971 AR060749 AR070434 AR103431 I13754 RABIL8RSB HSHAIL8G HSXDPB HSCKRL2 IJ HSU11870 HSU32674 X68149 Homo sapien X68829 H.sapiens m AP000909 Homo sapi E11245 Human cDNA AP000877 Homo sapi AP002357 Homo sapi AP002357 Homo sapi AP01357 Homo sapi X91116 M.mulatta M AX281745 Sequence X91113 P.troglodyt X91112 M.mulatta M M74240 Oryctolagus M82873 Oryctolagus X65858 H.sapiens U11870 Human inter AR015971 Sequence AR060749 Sequence AR070434 Sequence AR103431 Sequence I13754 Sequence 6 I24456 Sequence 5 I3755 Sequence 5 I3755 Sequence 8 M94582 Human Inter AR107999 Sequence AR1107999 Sequence AR151870 Sequence AR107998 Sequence X71788 M.musculus L19593 Homo sapien G28560 human STS S U11869 Human inter M73969 Human inter Z79783 H. sapiens G U32674 Human orpha AR117009 Sequence X95876 H. sapiens m AF223642 Rattus no AB003174 Mus muscu AC105645 Rattus no X71463 R.norvegicu AL590763 Homo sapi Z79783 H.sapiens G Description

ALIGNMENTS

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KEYWORDS SOURCE	VERSION	ACCESSION		DEFINITION	LOCUS	HSXDPB/c	RESULT 1
HTG.	AL590763.1 GI:13751778	AL590763 AJ239319	region GJB1-DXS559 map Xq13.1, complete sequence.	om 6	HSXDPB 271144 bp DNA linear PRI 17-JUN-2001		

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AlaPheLeuProAlaLeuTyrSerLeuLeuPheLeuLeuGlyLeuLeuGlyAsnGlyAla
                                                                                                    SerAspSerCysCysThrSerProProCysProGlnAspPheSerLeuAsnPheAspArg
                                                                                                                                                                                                                                                                                                                                                                                                                     Scores:
                    ValAlaAlaValLeuLeuSerArgArgThrAlaLeuSerSerThrAspThrPheLeuLeu 140
                                                                                                                                       GCCGAGGTTGCCGCCCTCCTGGAGAACTTCAGCTCTTCCTATGACTATGGAGAAAAACGAG
                                                                                                                                                                                   ACAGCCCCTTCCTCCCCGTTCCCGCCCTCACAGGTGACCACCCAAGTGCTAAATGAC
                                                                                          AGTGACTCGTGCTGTACCTCCCCGCCCTGCCCACAGGACTTCAGCCTGAACTTCGACCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (15-FEB-1999) MPING, Abt.Lehrach, Max Planck Fuer Molekulare Genetik, Ihnestrasse 73, Berlin, 14195 Bases 1.5000 overlap with AL590762 (HSXDPA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ramser,J., Heitmann,K., Sudbrak,R., Kosiura,A., Klages,S., Steffens,C., Borzym,K., Kube,M., Lehrack,S., Marquardt,I., Schuelzchen,S., Starke,A., Thompson,C., Hennig,S., Francis, Nemeth,A., Monaco,A., Lehrach,H. and Reinhardt,R.
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(bases 1 to 271144)
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/clone="PAC RPCI-1 56F19"
/clone=1ib="RPCI1,3-5 Human PAC library, or institute; Roswell Park Cancer Institute, Cr de Jong, P. Ioannou"
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/db_xref="taxon:9606"
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59391 c 63906 g 76614 t
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                         Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
1 (bases 1 to 1563)
Gutterrez, ... Varona, R., Zabal
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Z79783
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Catarrhini;
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AsnPheTyrAlaGlyAlaLeuLeuLeuAlaCysIleSerPheAspArgTyrLeuAsnIle
                                           AlaValGlnTrpValPheGlySerGlyLeuCysLysValAlaGlyAlaLeuPheAsnIle
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                                 GCCGTCCAGTGGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGTGCCCTCTTCAACATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zaballos,A.

Direct Submission

Direct Submission

Submitted (03-SEP-1996) Angel Zaballos, Research,

Submitted (03-SEP-1996) Angel Zaballos, Research,

Upjohn, Antonio Lopez 109, Madrid, 28026, Spain

Location/Qualifiers
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AVQWYFGSGLCKVAGALFAININFYAGALLLACISFDTFILHLAVADTLTVGFPPARVTLT
CLAVWGLCLLFALPDFIFLSAHHDERLNATHCQVNFPQVGRTALRVLQLVAGFILPLL
VMAYCYAHILAVLUSGGRRURAMRLIVVVVVVAFALCWTPYHLVVLVDILMDLGALA
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RQPSSSRRDSSWSETSEASYSGL"
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/db_xref="taxon:9606"
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                                                                                                                                                                                                              Human orphan
U32674
U32674.1 GI:
Marchese,A., Heiber,M.; Nguyen,T., Heng,H.H.Q., Saldivia,V.R., Cheng,R., Murphy,P.M., Tsui,L.-C., Shi,X., George,S.R., O'Dowd,B and Docherty,J.M.
Direct Submission
Submitted (31-JUL-1995) B.F. O'Dowd, Department of Pharmacology, University of Toronto, 8 Taddle Creek Rd., Toronto, Ontario MSS
                                                                      and GPR14, encoding receptors related to in
neuropeptide Y, and somatostatin receptors
Genomics 29 (2), 335-344 (1995)
96115583
                                                                                                            and Docherty, J.M.
Cloning and chromosomal mapping
                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 1293)
Marchese, A., Heiber, M., Nguyen, T., Heng, H.H.Q., Sald Cheng, R., Murphy, P.M., Tsui, L.-C., Shi, X., George, S.
                                                                                                                                                                                  Homo sapiens
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/db_xref="G1:1002741"
/db_xref="G1:1002741"
/tanalation="vsbHqVLNDAEVAALLENFSSSYDYGENESDSCCTSPPCPQDFS
LNFDRAFLPALYSLLFLIGLLGNGAVAAVLLSRRTALSSTDTFLLHLAVADTLLVLTL
LNFDRAFLPALYSLLFLIGLLGNGAVAAVLLSRRTALSSTDTFLLHLAVADTLLVLTL
LNADAAVQNVFGSGLCKVAGALFNLMFYAGALLLACISFDRYLNYVHATQLYRRGP
PARWTLTCLAVNGLCLLFALPDFIFLSAHDFLNATHCQYNFPQVGRTALRVLQVVA
GFLLPLLVMAYCYAHLLAVLLVSRGQRRLRAMEILVVVVVVAFALCWTPYHLVVLVDIL
GFLLPLLVMAYCYAHLLAVLLVSRGQRRLRAMEILVLXFVGVKFRERMWMLLLRLGC
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/codon_start=1
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/chromosome="8"
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Sequence
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Loetscher,M. and Moser,B.
Method of detecting or identifying ligands, inhibitors of CXC chemokine receptor 3
Patent: US 6140064-A 1 31-OCT-2000;
Location/Qualifiers
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ValGlyArgThrAlaLeuArgValLeuGlnLeuValAlaGlyPheLeuLeuProLeuLeu
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                                                                                                     ArgLeuArgAlaMetArgLeuValValValValValValAlaPheAlaLeuCysTrpThr
                                                                                                                             GTCATGGCCTACTGCCCACACCTCCTGGCCGTGCTGCTTTCCAGGGGCCAGCGG
                                                                                                                                     ValMetAlaTyrCysTyrAlaHisIleLeuAlaValLeuLeuValSerArgGlyGlnArg
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Submitted (26-FEB-1996) M. Loetscher, Theodor-Kocher Institute,
University of Bern, Freiestrasse 1, CH-3012 Bern, SWITZERLAND
Location/Qualifiers
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Loetscher,M., Gerber,B., Loetscher,P., Jones,S.A., Clark -Lewis,I., Baggiolini,M. and Moser,B. Chambkine receptor specific for IP10 and mig: structure and expression in activated T-lymphocytes
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LVAGFLMPLLVMAYCYAHILAVLLVSRGQRRFRAMRLVVVVVVAFAVCWTPYHLVVLV
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LVAGFLLPLIVMAYCYAHILLVUSRGQRKRRAMRLVVVVVAAFAYCWTPYHLVVLV
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/tissue_type="blood"
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Submitted (27-JAN-1998) Immunobiology,
California Ave., Palo Alto, CA 94304,
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Eukaryota; M
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
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DFSLNFORTFILPALYSLLFLLGILIGNGA/VAAVLLSQRFALSSFDTFILLHLAVADVLLV
LTLPLMAVDAAVQMVFGFGLGKVAGALLFNINFYAGAFILLACISFDRYLSIVHATQIYR
RDPRVRVALTCIVVWGLCLLFALPDFIYLSANVDQRLNATHCQYNFPQVGRTALEVLQ
LIVAGFILPLLVMAYCVAHILAVLLVSRCQRRFRAMRLVVVVVAAFAVCWTPYHLVVLV
DILMGFULPLLVMAYCVAHILAVLLVSRCQRRFRAMRLVVVVVAAFAVCWTPYHLVVLV
DILMDVGVLARNCGRKSHVDVAKSVTSGMGYMHCCLNPLLYAFVGVKFREKMWMLFTR
LGRSDQRGPQRQPSSSRRESSNAETTEASYLGL"

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/product="chemokine re
/protein_id="AAC40163.
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1 (bases 1 to 262652)

Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Banks,T., Barbaria,J.,
Benton,J., Bimage,K., Blankenburg,K., Bonnin,D., Bouck,J.,
Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P., Buhay,C.,
Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C., Carron,T.F.,
Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R.,
                                                                                                    Rattus norvegicus
Eukaryota; Metazoa;
Mammalia; Eutheria;
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AC105645.1 GI:18092868
HTG; HTGS_PHASE1; HTGS_DRAFT
                                                                                                                                             Norway
                                                                                                                                                                                             Rattus norvegicus chromosome DRAFT SEQUENCE, 75 unordered
                                                                                           Rattus.
                                                                                                    Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                           bp DNA linear HTG 09-JAN
Iddm4 clone CH230-205K13, WORKING
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Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Elagar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Elagar, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hakes, A., Hernandez, J., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B., Homsi, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivett, S., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L. Ci., J., Liu, X., Lucier, A., Lucier, R., Luna, R., Martinez, E., Massey, E., Mawhiney, E., McLeod, M., P., Meador, M., Morgan, M., Morris, S., Moser, M., Neal, D., Newtson, J., Newtson, N., Netzker, M., Muyeen, N., Noser, M., Neal, D., Newtson, J., Newtson, M., Nugyen, A., Nguyen, N., Nickerson, E., Putlins, M., Ren, Y., Rives, M., Oviedo, R., Pace, A., Payton, B., Peery, J., Peters, L., Peters, L., Pickens, R., Primus, E., Putli, L., Quiles, M., Ren, Y., Rives, M., Sonaike, T., Sparks, A., Stanley, H., Stone, H., Shoshtari, N., Savatek, A., Tabor, P., Tamerisa, K., Tamerisa, K., Tamerisa, K., Tamerisa, K., Tamerisa, K., Martington, S., Ward, Moore, S., Warren, R., Washington, C., Wall, R., Wang, S., Ward, Moore, S., Warren, R., Washington, C., Weilshon, C., Wolfer, S., Warren, R., Washington, C., Weilshon, D., Vinson, R., Wall, R., Wooden, S., Weilson, D., Weilshon, D., Willeon, D., Williams, G., Williamson, A., Wleczyk, R., Wooden, S., Weilson, D., Weilson, D., Williams, G., Williamson, A., Wleczyk, R., Wooden, S., Weilson, D., Weilson, D., Weilson, D., Weilson,
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Submitted (09-JAN-2002) Human Genome Sequencing of Molecular and Human Genetics, Baylor College Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             findPhrapList
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2 (bases 1
                                                                                                                                                           (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 75 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Center project name: GNKV
Center clone name: CH230-205K13
----- Summary Statistics
Assembly program: Phrap; version
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15232: contig of 15232 bp in
15332: gap of unknown length
27159: contig of 11827 bp in
27259: gap of unknown length
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TITLE
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AUTHORS
TITLE

JOURNAL

COMMENT

36908: 37008: 46032: 46132:

gap of contig

of 9649
unknown
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of 9749
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122561: 122661: 127209: 127309: 127314: 132014: 132014:

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136744: 140746:

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f unknown
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                                                              Submitted (30-JUN-1993) M. Kouba, Dept. of Phymunich, Pettendoferstrasse 12, D-8000 Muenchen
                                                                                                                                                               Kouba,M., Vanetti,M., Wang,X., Schafer,M. and Cloning of a novel putative (5.2) contains coupled is expressed in neuronal and lymphatic tissue FEBS Lett. 321 (2-3), 173-178 (1993)
                                                                                                                                                                                                                                                                                                                                                                            NRGPCNLR 1236 bp DNA R.norvegicus m RNA for G-Protein-coupled
                                                                                                                     Kouba, M
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/db_xref="taxon:10116"
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Rodentia; Sciurognathi; Muridae;
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CGCCGTCTCCTCTATCCACATCACCTGCTCGACTATTTGGCTAGCCGGCTTCCTATTT
                              {\tt GlyProProAlaArgValThrLeuThrCysLeuAlaValTrpGlyLeuCysLeuLeuPhe}
                                                              GCCTGCATAGCTGTCGACCGTTATCTGGCCATCGTCCATGCGGTCCACGCCTACCGCCGC
                                                                                                                             CTCTGCAAAAACTGTGATCGCCCTGCACAAGATCAATTTCTACTGCAGCAGCCTGCTGCTG
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58. .1125
/gene="rNLR"
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/db_xref="GI:599927"
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Gunn, M.Dee, Williams, L.T. and Cyster, J.G.
Modulating the interaction of the chemokine,
Hemoattractant, and its Receptor, BLR1
Patent: US 6116695-A 5 29-AUG-2000;
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M.musculus blr-1
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1 (bases 1 to 2517)
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379. .441
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172. .234
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TSRFLYHIGGFLLPWLVMGWCYVGVVHRLLQAQRRPQRQKAVRVAILVTSIFFLCWSP
YHIVIFLDTLERLKAVNSSCELSGYLSVAITLCEFLGLAHCCLNPMLYTFAGVKFRSD
                                                                                                                       /number=3
508. .570
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58. .>2517
                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="swiss-proj:004683"
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VEILPFAVAEGSYGMVLGTFLCKTVIALHKINFYCSSLLVACIAVDRYLAIVHAVHAY
                                                                                                                                                                                                                                                                      /gene="blr-1"
/note="transmembrane;
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/tissue_type="liver"
/clone_lib="mouse genomis
/dev_stage="adult"
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Am Klopferspitz 18a, D-82152 Martinsried, FRG
1997 this sequence version replaced gi:433946.
Location/Qualifiers
                                                                                       /gene="blr-1"
/note="putative;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /protein_id="CAA50673.1"
/db_xref="GI:433947"
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/strain="Balb/c"
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                                                                                                                                  ArgValLeuGlnLeuValAlaGlyPheLeuLeuProLeuLeuValMetAlaTyrCysTyr 282
                                                                                                                                                                                                                                                                                                                     GlyProProAlaArgValThrLeuThrCysLeuAlaValTrpGlyLeuCysLeuLeuPhe
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AGGGTGGCCATTTTAGTGACAAGCATTTTCTTCCTCTGCTGGTCGCCCTACCACATTGTC
                                                           GTGGGCGTGGTCCACAGGCTACTGCAGGCCCCAGCGGCGCCCTCAGCGGCAGAAGGCGGTC
                                                                                                                                                                                                           AlaThrHisCysGlnTyrAsnPheProGlnValGlyArgThr-----AlaLeu
                                                                                                                                                                                                                                       GCCTTACCGGAACTCCTCTTTGCCAAGGTTGGCCAACCTCATAACAACGACTCCTTA---
                                                                                                                                                                                                                                                                     AlaLeuProAspPheIlePheLeuSerAla-----HisHisAspGluArgLeuAsn
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                                                                                   AlaHisIleLeuAlaValLeuLeu---ValSerArgGlyGlnArgArgLeuArgAlaMet 301
                                                                                                                    CGTTTCCTCTACCACATCGGGGGCTTCCTACTACCGATGCTTGTGATGGGATGGTGTTAC
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2435. .2440
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922. .987
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/note="transmembrane;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sprenger,H., Lloyd,A.R., Lautens,L.L., Bonner,T.I. and Kelvin,D.J. Structure, genomic organization and expression of the human interleukin-8 receptor B gene J. Biol. Chem. (1994) In press
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Homo sapiens interleukin 8 receptor
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            /db_xref="GDB:G00-127-868"
/translation="MEDENMESDSFEDEWKGEDLSNYSYSSTLPPFLLDAAPCEPESL
/translation="MEDENMESDSFEDEWKGEDLSNYSYSSTLPPFLLDAAPCEPESL
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LVKFICLSIWGLSLLLALPVLLFRRTYVSSRVSPACYEDMGNNTANWRMLLRILPQSF
GFIVPLLIMLFCCYGFTLRTLFKAHMGQKHRAMRVIFAVVLIFLLCWLPYNLVLLADTL
MRTQVIQETCERRNHDDRALDATEILGILHSCLNPLIYAFIGQKFRHGLLKILAIHGL
                                                                                                                                          /gene="IL8RB"
/codon_start=1/
/product='interleukin 8 receptor beta"
/protein_id="AAB59437.1"
/db_xref="GI:559054"
                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
/map="2"
                                                                                                                                                                                                                                                                                                                                                      /gene="IL8RB"
/note="full length; G00-127-868"
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                                                                                                                                                                                                                                                                                                         'gene="IL8RB"
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beta (IL8RB) mRNA, complete
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                                                                 AACATGGAGAGTGACAGC------TTTGAAGATTTCTGGAAAGGTGAAGAT 465
                                AlaLeuSerSerThrAspThrPheLeuLeuHisLeuAlaValAlaAspThrLeuLeuVal 150
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G28560
G28560.1
STS; STS
                                       Eukaryota; Metazoa; Chordata;
Mammalla; Eutheria; Primates;
1 (bases 1 to 2856)
Myers;R.M.
     Contact: Richard M. Myers
                            Unpublished
                                                                                          Homo sapiens
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STS SHGC-35278, sequence tagged:
                                                                                                                 sequence; primer; sequence
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                                                               Craniata; Vertebrata; Catarrhini; Hominidae
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Best Local Similarity:
Query Match:
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                                                                                                                                                         ProGlyLeuTyrThrAlaProSerSerProPhePro---ProSerGlnValSerAspHis
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ProGlnAspPheSerLeuAsnPheAspArgAlaPheLeuProAlaLeuTyrSerLeuLeu 110
                             CTTAGTAATTACAGTTACAGCTCTACCCTGCCCCCTTTTCTACTAGATGCCGCCCCATGT
                                                       SerSerSerTyrAspTyrGlyGluAsnGluSerAspSerCysCysThrSerProProCys
                                                                                    AACATGGAGAGTGACAGC-----
                                                                                                              GlnValLeuAsnAspAlaGluValAlaAlaLeuLeuGluAsnPhe----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Stanford Human Genome Center (SHGC)
Stanford University School of Medicine
Department of Genetics, M-344, Stanford,
Tel: 4157259687
Fax: 4157259689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Primer A: ACATTCCAAGCCTCATGTCC
Primer B: CTTAGAACATAGAGTGCCATGGG
STS size: 217
PCR Profile:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Prepared with primer pairs provided by Sandoz, -- Washington University/Merck EST sequence.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                            755
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Taq Polymerase:
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KCl:
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                                                                                                                                         -CCAGCGACCCAGTCAGGATTTAAGTTTACCTCAAAAATGGAAGATTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
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ACCESSION U11869 VERSION U11869.1 GI:511801 KEYWORDS .	RESULT 15 HSIL8RB4 LOCUS HSIL8RB4 LOCUS HUman interleukin-8 receptor type B (IL8RB) gene, exons 10 and 11 and complete cds.	Qy 396 SerSerArgArgAspSerSerTrpSerGluThrSer 408	Qy 376 MetTrpMetLeuLeuArgLeuGlyCysProAsnGlnArgGlyLeuGlnArgGlnPro 395 :::	Qy 356 MetHisCysCysLeuAsnProLeuLeuTyrAlaPheValGlyValLysPheArgGluArg 375 :::	Qy 336 AsnCysGlyArgGluSerArgValAspValAlaLysSerValThrSerGlyLeuGlyTyr 355	Qy 316 ThrProTyrHisLeuValValLeuValAspIleLeuMetAspLeuGlyAlaLeuAlaArg 335	Qy 296 ArgArgLeuArgAlaMetArgLeuValValValValValValAlaPheAlaLeuCysTrp 315 Db 1141 CAGAAGCACCGGGCCATGCGGTCTTGCTGTCGTCCTGCTCTGCTGG 1200	276 LeuValMetAlaTyrCysTyrAlaHisIleLeuAlaValLeuLeuValSerArgGlyGln ::: ::: 1081 CTGATCATGCTGTTCTGCTACGGATTCACCCTGCGTACGCTGTTTAAGGCCCACATGGGG	259 1021	Qy 242 AspGluArgLeuAsnAlaThrHisCysGlnTyrAsnPheProGlnValGly 258 ::::::::::::::::::::::::::::::::::::	222 ValTrpGlyLeuCysLeuLeuPheAlaLeuProAspPheIlePheLeuSerAlaHisHis :::	Qy 211 ProProAlaArgValThrLeuThr	Qy 191 CysIleSerPheAspArgTyrLeuAsnIleValHisAlaThrGlnLeuTyrArgArgGly 210		Qy 151 LeuThrLeuProLeuTrpAlaValAspAlaAlaValGlnTrpValPheGlySerGlyLeu 170	Qy 131 AlaLeuSerSerThrAspThrPheLeuLeuHisLeuAlaValAlaAspThrLeuLeuVal 150	Qy 111 PheLeuLeuGlyLeuLeuGlyAsnGlyAlaValAlaAlaValLeuLeuSerArgArgThr 130
CDS	exon	exon	intror	mRNA	mRNA	mRNA		mRNA	mRNA	gene	mRNA		FEATURES SOUTCE	TITLE	JOURNAL MEDLINE REFERENCE AUTHORS	REFERENCE AUTHORS TITLE	SEGMENT SOURCE ORGANISM
/number=11 /evidence-experimental 11782260	မှ မြော်များ	/gene="IJ8RB" /gene="IJ8RB" /note="alternatively spliced variant IL8RB10, exons 10 and 11" 9721152	n <1971 /gene="IL8RB" /number=5 072	join(U11868.1:16168,11532847) /gene="IL8RB" /note="alternatively spliced variant IL8RB9, exons 9 and	join(Gil867.1:1671,11532847) /gene="IL8RB" /gene="alternatively spliced variant IL8RB7, exons 7,8 and	join(U11866.1:18161855,U11866.1:20772139, U11867.1:2071,11532847) /gene="TL8RB" /note="alternatively spliced variant IL8RB4, exons 4,6,8	<pre>/gene="IL8RB" /note="alternatively spliced variant IL8RB3, exons 3,5,6,8 and 11"</pre>	/note="alternatively spliced variant IL8RB2, exons 2,6,8 and 11"	.1568,U11866.1:20 32847)	<pre>/note="alternatively spliced variant IL8RB1, exons 1,6,8 and 11" join(U11866.1:10642253,U11867.1:188,U11868.1:1173, 12887)</pre>	ta" .1148,U11866.1:20772139, 32847)	/db_xref"taxon:9606" /db_xref"taxon:9606" /chromosome="2" /map="2q34-35" /filene="4"	=	Direct Submission Submitted (06-JUL-1994) Sunil K. Ahuja, Laboratory of Host Defenses, National Institutes of Health, National Institute of Allergy and Infectious Diseases, NIH, Bldg 10, Rm 11N109, Bethesda,	J. Biol. Chem. 269 (42), 26381-26389 (1994) 95014476 2 (bases 1 to 2847) Ahuia S.K.	1 to 2847) , Shetty,A., Tiffany,H.L. and Murphy,P.M. of the genomic organization and promoter frienkin-8 receptors A and B	4 of 4 human. Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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Percent Similarity:
Best Local Similarity:
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                                                                      TrpGlyLeuCysLeuLeuPheAlaLeuProAspPheIlePheLeuSerAlaHisHisAsp
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                                   TGGGGTCTGTCCTTGCCCTGCCCTGCCTGTCTTACTTTTCCGAAGGACCGTCTACTCA 1744
                                                                                                                                              ProAlaArgValThrLeuThr-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="IL8RB"
/note="neutrophil chemoattractant receptor"
/codon_start=1
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-WARN_TIMEOUT-30 -THREADS-1 -MGAPOP-10 -XGAPEXT-0.5 -FGAPOP-6 -FGAPEXT-7
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GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                        /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

RESULT 1

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CDS
                                                       HSATU68; G-protein chemokine receptor; 7-transmembrane receptor; signal transduction; gene therapy; diagnosis; ss.
                                                                                    Human G-protein chemokine receptor HSATU68 cDNA.
                                                                                                        28-SEP-1997
                                                                                                                           AAT72800;
                                                                                                                                            AAT72800 standard;
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Location/Qualifiers
173..1420
/*tag= a
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Alignment
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                                                                                                                                                                                                                                                                                                                                                                                               A cDNA clone (AAT72800) codes for a newly identified human chemokine receptor (AAW19780) designated HSATU68. It was in a human genomic library derived from activated T cells: nucleic acids be used to produce HSATU68 in prokaryotic or eukaryotic host cells, as probes for the detection, screeni diagnosis of diseases caused by mutations in the HSATU68 ge in the gene therapy of conditions related to underexpression receptor its ligand.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA encoding new isolated human G-protein chemokine recepto to develop products for treating, e.g. autoimmune diseases, infections, allergy, malignancy, inflammation or shock
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                                                                      AGTGACTCGTGCTGTACCTCCCCGCCCTGCCCACAGGACTTCAGCCTGAACTTCGACCGG
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                                    cancer; colon cancer antigen;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the proteins are collectively known as colon cancer antigens. The colon cancer antigens have cytostatic activity and can be used in gene therapy and vaccine production. N and P may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate P expression. For example, N and P may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of P by expressing inactive proteins or to supplement the patients own production of P. Additionally, N may be used to produce the colon cancer-associated Ps, by inserting the nucleic acids into a host cell and culturing the cell to express the proteins. N and P can be used in the prevention, diagnosis and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204 and AAB7789 represent sequences used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAH32943 to AAH371 cancer-associated the proteins are c
                                                                                                                                                                                                                                                                                                                                                                                                                                present invention.

N.B. Pages 666 to 682 and page 7053 of the missing at time of publication, meaning no SEQ ID NO:1027 to 1052, 7921 and 7922.
                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1877
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03-NOV-1999;
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                                                  ThrAlaProSerSerProPheProProSerGlnValSerAspHisGlnValLeuAsnAsp
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            SerAspSerCysCysThrSerProProCysProGlnAspPheSerLeuAsnPheAspArg 100
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bB; AAG75628.
                                                                                                       to AAH37195 and AAG73514 to AAG77788 represent human sociated nucleic acid molecules (N) and proteins (P).
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AAZ32713

ВP

31-JAN-2000 (fi Human chemokine

receptor CXCR3b cDNA.

(first entry)

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                                                                                                                        This sequence represents cDNA encoding human chemokine receptor CXCR3b, CC a splice variant of chemokine receptor CXCR3 (also referred to as CC CXCR3a). Chemokines are a family of small cytokines which bring about the recruitment of leukocytes during inflammation. The CXC chemokines CC mostly attract neutrophils, while the CC chemokines are less selective. All chemokine receptors are seven transmembrane G-protein coupled CC receptors and most are receptors for a number of chemokines, CXCR3a CC being a receptor for the CXC chemokines IP10 and Mig. CXCR3a is CC expressed in activated, but not in resting T-lymphocytes, and may CC therefore play an important role in the selective recruitment of CC T-cells which occurs in T-cell mediated inflammatory conditions. CC CXCR3b may have an altered pattern of tissue distribution and CC concion in the inflammatory process. Cells expressing the active CC CXCR3b may have an altered pattern of tissue distribution and CC continuities, of a chemokine receptor. In addition, the receptor CC citation of the complexity of the composition of chemokines responsible for mediating CC inflammation reactions via interaction with CXCR3b. The modulation CC inflammatory responses is of therapeutic benefit in many conditions CC can distington the receptor. In addition, delayed type hypersensitivity reactions, atherosclerosis and restenosis.
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                                                                                                                                                                                The mammalian CXC chemokine receptor 3 (CXCR3) gene encodes a protein which can selectively bind one or more chemokines and can mediate cellular signalling and/or a cellular response in response. Inhibitor and promoters of mammalian CXCR3 can be detected and identified using host cells expressing CXCR3. CXCR3 inhibitors can be used for treatment of inflammatory diseases which are T cell mediated. CXCR3 promoters
                                                                                                                                                                                                                                                                         which, are useful for treatment of i anti-viral therapy
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10-SEP-1996;
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P-PSDB; AAW54371.
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US-09-101-518A-2
                                          Percent Similarity:
Best Local Similarity:
Query Match:
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                                                                                                                                                                           acids N-terminal of an endogenous proline in TM6 to form a sequence

2 X-(AA)15 Pro. The endogenous amino acid is selected from Lys, His, Arg

3 cr Ala, and is preferably Lys. When the endogenous residue at this

3 cr Ala, and is preferably Lys. When the endogenous residue at this

3 cr Ala, and is preferably Lys. When the endogenous residue at this

3 cr Ala, and is preferably Lys. When the endogenous residue at this

3 cr Ala, and is preferably Lys. When the endogenous residue at this

4 cr Ala, and is preferably Lys. When the endogenous residue at this

5 cr Ala, and is preferably Lys. When the endogenous residue is replaced by His, Arg or preferably Ala.

5 cr Ala, and is preferably Lys. When the endogenous residue is residue at the Pro

6 cr Ala, and is preferably Lys. When the endogenous and the Pro

7 cr Ala, and is preferably Lys. When the endogenous and the Pro

8 cr Ala, and is preferably Lys. When the Pro

9 cr Halo and Ala Properties are useful for containing the second constitutively articular GPCR are useful for containing diseases and disorders associated with that receptor. Because the novel mutant GPCRs are constitutively active, they can be used the endogenous containing an exemplification of the invention. This was cloned and containing a mutant of the invention.

9 cr Ala, and is a preferably Lys. When the endogenous containing a mutant of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to constitutively active, non-endogenous versions of endogenous human orphan G protein-coupled receptors (GPCRs, AAY90643-AAY90677 and AAY90683-Y90687), and to DNA encoding them (AAA30709-A39743 and AAA30775-A30779). The mutant proteins of the invention contain a mutation in a portion of the protein comprising intracellular loop 3 (IC3) and transmembrane domain 6 (TM6). A non-endogenous amino acid, x, is substituted for an endogenous residue in IC3 at a position 16 amino
                                                                                                  No.:
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The invention relates to constitutively active, non-endogenous versions of endogenous human orphan G protein-coupled receptors (GPCR8, AAY90643-CC AAY90677 and AAY90683-Y90687), and to DNA encoding them (AAA30709-A30743 CC and AAA30775-A30779). The mutant proteins of the invention contain a CC mutation in a portion of the protein comprising intracellular loop 3 CC (IC3) and transmembrane domain 6 (7M6). A non-endogenous amino acid, X, is substituted for an endogenous residue in IC3 at a position 16 amino CC acids N-terminal of an endogenous proline in TM6 to form a sequence CC X-(AA)15-Pro. The endogenous amino acid is selected from Lys, His, Arg CC or Ala, and is preferably Lys. When the endogenous residue at this CC position is Lys, this residue is replaced by His, Arg or preferably Ala. CC The 15 amino acid stretch between the substituted amino acid and the Pro CC may be endogenous, non-endogenous, or a mixture of endogenous and con-endogenous residues. The constitutively active GPCR8 are useful for identifying antagonists, agonists and partial agonists for use as CC pharmaceutical agents. The mutant proteins are also useful in research constituing the roles of the receptors in normal and CC diseased conditions. Antagonists for a particular GPCR are useful for the novel mutant GPCRs are constitutively active, they can be used
 Percent Similarity:
Best Local Similarity:
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P-PSDB; AAY90648.
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                                                                                                the novel mutant GPCRs are constitutively active, they can directly for screening of compounds without the need for en ligands. Sequences AAA30709- AAA30743 and AAA30775-A30779 rencoding the mutant human GPCRs of the invention.
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                             or development e.g. inflammatory conditions such as asthma. Chemckines are important in immune and inflammatory responses in that they induce laukocyte migration and adhesion. They are also chemoattractants for several cells involved in inflammation and can induce other biological responses e.g. modulation of second messenger levels (e.g. Ca++), cellular morphology modification responses, phosphoinositide lipid turnover, possible antiviral responses etc. The chemokine receptors of the invention exhibit structural properties of G-protein coupled receptors (GPCR), although their ligands have not yet been identified. The chemokine and chemokine receptor polypeptides are useful to produce ligand: receptor complexes in vivo or in assay techniques. Assays may also involve chemical antagonists which block complex production or
                                                                                                                                                                                                                                      This represents a rodent chemokine receptor HST01.1 nucleotide sequence. The invention provides novel primate and rodent chemokines and chemokine receptors. The chemokines, receptors and binding compounds (optionally antibodies/fragments specifically binding the chemokines) are useful therapeutically to treat conditions associated with abnormal physiology of the property of the conditions associated with abnormal physiology.
                                                                                                                                                                                                                                                                                                                                                                         Rodent and primate chemokines and chemokine receptors - useful diagnostically and therapeutically to treat conditions associated with abnormal physiology or development e.g. inflammatory conditions
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ry response; immune response; leukocyte migration;
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The invention relates to identifying modulators of receptor activity using orthologues of human receptors by contacting a compound with receptors from two species, and measuring the effect of the compound on the receptors. Included is an isolated nucleic acid (I) comprising a nucleotide sequence encoding bradykinin B1 receptor (II); or encoding a CXCR2 receptor (III). The method is useful for identifying a compound having dual specificity to modulate the activity of a desired polypeptide in two different species. The method is useful for identifying a non-human animal model for testing compounds with potential efficacy as human receptor modulators. The method comprises contacting a test compound with receptors from at least two species; measuring an effect of the compound on the receptors; and selecting an animal model representing a species
                                                                                                                                                                                                                                                                                                                                                                                                                               Identifying modulators of receptor activity using orthologues of human receptors by contacting a compound with receptors from two species, an measuring the effect of the compound on the receptors -
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orangutan; gorilla; tree shrew; dog; analo
bradykinin 1 receptor; CXCR2 receptor; pa;
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CACATGGGGCAGAAGCACCGGGCCATGCGGGTCATCTTTGCTGTTGTCCTCATCTTCCTA 768
                 ArgGlyGlnArgArgLeuArgAlaMetArgLeuValValValValValValAlaPheAla
                                                                                         LeuProLeuLeuValMetAlaTyrCysTyrAlaHisIleLeuAlaValLeuLeuValSer
                                                                                                                         AACAATACAGCAAAATGGCGGATGGTGTGCGGATCCTGCCCCAGACCTTTGGCTTCATC
                                                                                                                                                                                                              AlaHisHisAspGluArgLeuAsnAlaThrHisCysGlnTyrAsnPheProGlnValGly
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                                                          TTGCCACTGCTGATCATGCTGTTCTGCTATGGATTCACCTTGCGCACGCTGTTTAAGGCC
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                                                                                                                                                                                  ACTGTCTACCCGACCTATATTAGCCCAGTC---TGC----TATGAGGACATGGGC
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                                                                                                                                                                                                                                                                                                         -ACACTGACCCAGAAGCGCTACTTGGTCAAGTTCGTA
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Mismatches:
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                      This is the nucleotide sequence of murine cDNA coding for a Burkitt's lymphoma receptor 1 (BLR1, see AAV06643). The invention relates to methods for modulating the interaction of BLR1 with its ligand, B lymphocyte chemoattractant (BLC, see AAV06641). The methods comprise combining BLR1 and BLC polypeptides with a candidate modulator agent under conditions whereby, but for the presence of the agent, the polypeptides engage in a first interation, and determining a second interaction of the polypeptides in the presence of the agent, wherein a difference between the first and second interactions indicates that the agent modulates the interaction of the polypeptides. The modulator is preferably an antagonist, especially dominant negative, form of
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             preferably an BLC. BLC and
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mphocyte chemoattractant; BLC; chemokin
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              BLC agonists and antagonists may be
(e.g.
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          ArgValAspValAlaLysSerValThrSerGlyLeuGlyTyrMetHisCysCysLeuAsn
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                                                                                                                                                           The invention relates to identifying modulators of receptor activity CC using orthologues of human receptors by contacting a compound with receptors from two species, and isolated nucleic acid (I) comprising a conceptors. Included is an isolated nucleic acid (I) comprising a conceptor (III). The method is useful for identifying a compound CC CXCR2 receptor (III). The method is useful for identifying a compound CC axing dual specificity to modulate the activity of a desired polypeptide in two different species. The method is useful for identifying a non-cc human animal model for testing compounds with potential efficacy as human creceptor modulators. The method comprises contacting a test compound with receptors from at least two species; measuring an effect of the compound con the receptors; and selecting an animal model representing a species chaving a receptor that exhibits the desired effect when contacted with the test compound. Also described is a method for identifying a compound contacted that modulates (II) or (III) activity, where a compound is an agonist, and inflammation and other receptor related methologies and apprises.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 49; Page 100-101; 108pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Identifying modulators of receptor activity using orthologues of human receptors by contacting a compound with receptors from two species, an measuring the effect of the compound on the receptors -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; baboon; chimpanzee; vervet monkey; rhesus macaque; orangutan; gorilla; tree shrew; dog; analgesic; antiinflammatory; bradykinin l receptor; CXCR2 receptor; pain; inflammation; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22-MAY-2001; 2001WO-US16777
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                                                                                                       and inflammation and other receptor related pathologies. ABK16569-
6574 and ABK16589-ABK16599 represent bradykinin 1 and CXCR2 recepto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2002-106172/14.
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                                                CACAGTGACATCAACCAGGCCCTGGATGCCACCGAGATTCTGGGCATCTTTCACAGCTGC
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                                         Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and sequences ABA08225-ABA09574 represent nucleic acids encoding them. The invention also relates to vectors and recombinant host cells comprising a nucleotide of the invention, methods of producing the novel polypeptides, antibodies against the polypeptides, methods of identifying compounds which bind to polypeptides in a sample, and methods of identifying compounds which bind to polypeptides of the invention Although novel, many of the polypeptides of the invention have homology to known proteins, thereby glving an insight into their probable biological activities, and hence potential therapeutic applications. The polypeptides of the invention may have various activities, including cytokine, cell proliferation or cell differentiation activities, stem cell growth factor activity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        myeloid cell disorder; lymphoid cell disorder; asthma; arthritis; chronic inflammatory condition; proliferative retinopathy; atherosclerosis; coronary heart disease; arterial ischaemia; bone disorder; osteoporosis; vascular growth disorder; tissue regeneration; wound healing; infection; immune disorder; cell culture; drug screening; gene therapy; antiinflammatory; antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic; cytostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1030
                                                                                                                                                                                                                                                                     Claim 1; Page 874; 1963pp;
                                                                                                                                                                                                                                                                                                   treating or ame e.g. arthritis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          03-FEB-2000; 2000US-0496914
27-APR-2000; 2000US-0560875
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           haematopoiesis regulation; tissue growth; immunomodulator; activin; inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis; proliferation; metastasis; cancer; tumour; haematopoietic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human IL-8R B homologue-encoding cDNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABA09268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABA09268 standard;
                                                                                                                                                                                                                                                                                                                      Human proteins and DNA encoding sequences useful for preventing, treating or ameliorating a medical condition in a mammalian subject
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-JAN-2002
             haematopoiesis regulatory activity; tissue growth activity; immunomodulatory activity; activin- or inhibin-related activities;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HYSE-) HYSEQ INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cytokine; cell proliferation; cell differentiation;
                                                                                                                                                                                                                                                                                                                                                                          ABB12024.
                                                                                                                                                                                                                                                                                                                                                                                                                          Liu C,
                                                                                                                                                                                                                                                                                                                    ameliorating
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haemostatic,
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US-09-101-518A-2 (1-415) x ABA09268
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alignment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CC involved in oncogenesis, cancer cell proliferation or metastasis.

CC Depending on their biological activities, polypeptides and nucleotides of the invention are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Such conditions include cc cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell conditions, ceronic inflammatory conditions (e.g., asthma or arthitis), croliferative retinopathy, atherosclerosis, coronary heart disease, carterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal cc vascular growth. Polypeptides involved with tissue regeneration and crepair (or nucleic acids encoding them) may be used to promote wound healing (e.g., of burns, incisions and ulcers), while those with conditions are disorders.

CC bacterial and fungal infections in addition to immune disorders.

CC Polypeptides with growth factor activity may be used in cell cultures to promote cell growth. For example, such polypeptides may be used to manipulate stem cells in culture to give rise to neuroepithelial cells that can be used to augment or replace cells damaged by illness, can autoimmune disease or accidental damage. The polypeptides and nucleotides can status to ease of the above conditions, and in drug covel human polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  thrombolytic activities;
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CysIleSerPheAspArgTyrLeuAsnIleValHisAlaThrGlnLeuTyrArgArgGly
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                                                                                                      CysLysValAlaGlyAlaLeuPheAsnIleAsnPheTyrAlaGlyAlaLeuLeuLeuAla
                                                                                                                                                 CTGACCTTGCCCATCTGGGCCGCCTCCAAGGTGAATGGCTGGATTTTTTGGCACATTCCTG
                                                                                                                                                                                        LeuThrLeuProLeuTrpAlaValAspAlaAlaValGlnTrpValPheGlySerGlyLeu
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                                                              TGCAAGGTGGTCTCACTCCTGAAGGAAGTCAACTTCTATAGTGGCATCCTGCTACTGGCC
                                                                                                                                                                                                                                   GGCCGCTCCGTCACTGATGTCTACCTGCTGAACCTAGCCTTGGCCGACCTACTCTTTGCC
                                                                                                                                                                                                                                                                                                                    TTCCTGCTGAGCCTGCTGGGAAACTCCCTCGTGATGCTGGTCATCTTATACAGCAGGGTC
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Conservative:
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 Drmanac RT,
                                                                          31-MAR-2000;
23-AUG-2000;
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                                                                                                                                                                       11-OCT-2001
                                                                                                                                                                                                            WO200175067-A2
                                                                                                                                                                                                                                                                                 Human; chromosome mapping; gene mapping; gene therapy; forensic
food supplement; medical imaging; diagnostic; genetic disorder;
                                                                                                                                                                                                                                                                                                                                          DNA encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAS77796 standard; cDNA;
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                                                                            2000US-0540217.
2000US-0649167.
                                                                                                                                                                                                                                                                                                                                        novel human diagnostic protein #13600
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 Liu C,
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) Is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID No 13600; 103pp; English
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P-PSDB; ABG13609.
                                   131 AlaLeuSerSerThrAspThrPheLeuLeuHisLeuAlaValAlaAspThrLeuLeuVal 150
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                                                                                                                                                                                                                                                                                                                      AACATGGAGAGTGACAGC
                                                                                                              PheLeuLeuGlyLeuLeuGlyAsnGlyAlaValAlaAlaValLeuLeuSerArgArgThr 130
                                                                                                                                                                                                                                                                   SerSerSerTyrAspTyrGlyGluAsnGluSerAspSerCysCysThrSerProProCys
                 GGCCGCTCCGTCACTGATGTCTACCTGCTGAACCTAGCCTTGGCCGACCTACTCTTTGCC
                                                                                                                                                                   GAACCAGAA - - - TCCCTGGAAATCAACAAGTATTTTGTGGTCATTATCTATGCCCTGGTA
                                                                                                                                                                                                                                              CTTAGTAATTACAGTTACAGCTCTACCCTGCCCCCTTTTCTACTAGATGCCGCCCCATGT
                                                                                                                                                                                                                                                                                                                                                        GlnValLeuAsnAspAlaGluValAlaAlaLeuLeuGluAsnPhe------
                                                                                                                                                                                                                                                                                                                                                                                               ------CCAGCGACCCAGTCAGGATTTAAGTTTACCTCAAAAATGGAAGATTTT
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haplotyping; haplotype pair; single nucleotide polymorphism; genotyp gene therapy; drug screening; chronic obstructive pulmonary disease; inflammatory disease.
                                                                                               Human; interleukin 8 receptor beta; IL8RB;
                                                                                                                                                              14-FEB-2002
                       sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                             MetHisCysCysLeuAsnProLeuLeuTyrAlaPheValGlyValLysPheArgGluArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTGCCCTACAACCTGGTCCTGCCTGGCAGACACCCTCATGAGGACCCAGGTGATCCAGGAG
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                                                                                                                                                                                                                                                                                     AGGCCTTCCTTGTTGGCTCTTCTTCAGGGCACACTTCC
                                                                                                                                                                                                                                                                                                                 SerSerSerArgArgAspSerSerTrpSerGluThrSer
                                                                                                                                                                                                                                                                                                                                                 CTCCTCAAGATTCTAGCTATACATGGCTTGATCAGCAAGGACTCCCTGCCCAAAGACAGC
                                                                                                                                                                                                                                                                                                                                                                             MetTrpMetLeuLeuArgLeuGlyCysProAsnGlnArgGlyLeuGlnArgGlnPro
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                                                                                                                              interleukin 8 receptor
                                                                                                                                                                                                                          standard;
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                                                                                                                                                                                                                          DNA;
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                                                                                                                              beta (IL8RB) genomic
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      The invention relates to single nucleotide polymorphisms in the human interleukin 8 receptor beta (ILBRB) gene. A method for haplotyping the ILBRB gene in an individual comprises identifying the nucleotide at one or more polymorphic sites and determining whether one of the copies of the gene is defined by one of the ILBRB haplotypes given in the specification or whether both copies are defined by a haplotype pair. This method is useful in genotyping, whereby all possible haplotype pair can be assigned to specific genotypes. An association between a trait are
                                                                                                                                                                                      New polymorphic variants comprising isogene, useful in expressing ILBRB candidate drugs to treat diseases re
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replace(10612,T)
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the specification"
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                                                                                                                                                                                         ng interleukin-8 receptor beta RB protein for use in screening related to IL8RB activity, e.g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   a haplotype or haplotype pair of the IL8RB gene can be identified by comparing the frequency of the haplotype or haplotype pair in a population exhibiting the trait with the frequency of the haplotype or haplotype pair in a reference population, where a higher haplotype or haplotype pair. IL8RB and its corresponding DNA are used for studying the expression and function of IL8RB for use in screening for candidate drugs to treat diseases related to IL8RB activity, such as chronic obstructive pulmonary disease and other inflammatory disorders. The sequences are also useful for studying the effect of variation on the biological activity of IL8RB as well as on the binding affinity of candidate drugs targeting IL8RB. This sequence represents genomic DNA encoding TL8RB.
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                                                            LysValAlaGlyAlaLeuPheAsnIleAsnPheTyrAlaGlyAlaLeuLeuLeuAlaCys
                                                                                                                                                                                                                                                                                                                                                    ThrLeuProLeuTrpAlaValAspAlaAlaValGlnTrpValPheGlySerGlyLeuCys 171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTGCTGAGCCTGCTGGGAAACTCCCTCGTGATGCTGGTCATCTTATACAGCAGGGTCGGC 9808
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                                                                                             TrpGlyLeuCysLeuLeuPheAlaLeuProAspPheIlePheLeuSerAlaHisHisAsp 242
                                                                                                                              -----ACACTGACCCAGAAGCGCTACTTGGTCAAATTCATATGTCTCAGCATC
                                                                                                                                                               ProAlaArgValThrLeuThr----
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TCCAATGTTAGCCCAGCC---TGC-----TATGAGGACATGGGCAACAATACAGCA 10186

The invention relates to identifying modulators of receptor activity using orthologues of human receptors by contacting a compound with

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                                                                                                                                                                                                                                                                                                                        Human; baboon; chimpanzee; vervet monkey; rhesus macaque;
orangutan; gorilla; tree shrew; dog; analgesic; antiinflammatory;
bradykinin 1 receptor; CXCR2 receptor; pain; inflammation; ds.
                                Claim 49; Page 98-99;
                                                        Identifying modulators of receptor activity using orthologues of human receptors by contacting a compound with receptors from two species, and measuring the effect of the compound on the receptors \cdot
                                                                                                         WPI; 2002-106172/14.
P-PSDB; AAU80489.
                                                                                                                                            Horlick R,
Auld DS;
                                                                                                                                                                                                                                                                            WO200190134-A1
                                                                                                                                                                                                                                                                                                                                                                        DNA encoding rhesus macaque CXCR2 receptor
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GAGGACATGGGCAACAATACAGCAAAATGGCGGATGGTGTTGCGGATCCTGCCCCAGACC
                                                 ---GlnValGly----
                                                                                                                                                                                                CysLeuAlaValTrpGlyLeuCysLeuLeuPheAlaLeuProAspPheIlePheLeuSer
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                                                                                                                             AlaHisHisAspGluArgLeuAsnAlaThrHisCysGlnTyrAsnPhePro----
                                                                                                                                                                        SerGlyLeuCysLysValAlaGlyAlaLeuPheAsnIleAsnPheTyrAlaGlyAlaLeu ::: |||||||||||
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635.50
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                                                                                     -CGAAGGACTGTCTACCTGACCTATATTAGCCCAGTCTGCTAT
                                                                                                                                                                                                                                                             ----ACACTGACCCAGAAGCGCTACTTGGTCAAGTTCGTA
                                            ·----ArgThrAlaLeuArgValLeuGlnLeuVal
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QΥ

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09-JUL-1991;
09-DEC-1991;
Rabbit high affinity IL-8 receptor gene was isolated from ral peritoneal neutrophils and used as a source of poly(A)+ RNA,
                                     Disclosure;
                                                                                                                                                                                                                                                                                                                                  CDS
                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence encodin (IL-8) receptor
                                                            Recombinant mammalian interleukin-8 binding
                                                                                                             WPI; 1992-382123/46.
                                                                                                                                    Navarro J,
                                                                                                                                                                                                                                                                                                                                                                      Homo
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                                                                                                                                                                       REPLIGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                  encoding a low affinity recombinant human eceptor polypeptide in 4AB.
                                    Fig 2; 71pp; English.
                                                                                                                                    Thomas KM,
                                                                                                                                                             BOSTON
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                                                                                                                                                                                             91US-0685101.
91US-0726606.
91US-0803842.
                                                                                                                                                                                                                                                                                                                                                                                           polypeptide; G-protein-coupled receptor; ss
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                                                            interleukin-8 receptor - used for screening
antagonists, used to treat inflammation
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TTCCGAAGGACCGTCTACTCATCCAATGTTAGCCCCAGCC---TGC----TATGAG
                                     PheLeuSerAlaHisHisAspGluArgLeuAsnAlaThrHisCysGlnTyrAsnPhePro
                                                                                                                                                                      CGC---
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                                                CAGAAGTTTCGCCATGGACTCCTCAAGATTCTAGCTATACATGGCTTGATCAGCAAGGAC 1026
                                                                                                 GACATGGGCAACAATACAGCAAACTGGCGGATGCTGTTACGGATCCTGCCCCAGTCCTTT
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-Q-/cgn2_1/USPTO_spool/USO9101518/runat_29102002_091103_98/app_query.fasta_1.583
-DB-EST -OFMT-fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM-ext -HEAPSIZE=500 -MINLEN0 -MAXLEN=2000000000
-USER-USO9110518_GCGN_1_1/763_erunat_29102002_091103_98 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARR_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
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Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11510 row: c column: 01 Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, 1 (bases 1 to 851)
NHI-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D. mRNA sequence. BI768435 Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; Homo sapiens EST BI768435.1 GI:15760013 603053902F1 NIH_MGC_122 human. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium Homo sapiens cDNA 851 đđ Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo. mRNA clone IMAGE:5203512 linear EST 25-SEP-2001 GE:5203512 5', (LLNL)

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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies,
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1 (bases 1 to 864)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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                                                                                                                                                          /note="Vector: PCMV-SPORT6; Site_1: Not1; Site_2: EcoRV (destroyed); RNA source leukocytes from anonymous pool of non-activated adult donors. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range 1.2-3.3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 027. Note: this is a NIH MGC Library."
                                                                                                                                                                                                                                                                                                                                        /tissue_type="leukocyte"
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/clone_lib="NIH_MGC_118"
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/db_xref="taxon:9606"
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 749)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collect
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Contact: Robert St
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                                                                                                                                                                                                         Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and all
v0.980904.e. Vector identified by cross_matc
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Eukaryota;
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Sequence evaluation of four pooled-tissue normalized bovine libraries and construction of a gene index for cattle
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FORWARD: AGGAAACAGCTATGACCAT
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  /note="Vector: pCMV SPORT6; Site_1: xbaI; Site_2: xh Library made from pooled tissue from testis, thymus, semitendonosus muscle, longissimus muscle, pancreas, adrenal and endometrium "
                                              /tissue_type="pooled"
/lab_host="DH10B"
                                                                      /organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="MARC 2BOV"
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Bos taurus
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ThrGlnLeuTyrArgArgGlyProProAlaArgValThrLeuThrCysLeuAlaValTrp
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Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R. Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennet, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. a Keele, J.W.

Sequence evaluation of four pooled-tissue normalized bovine cF libraries and construction of a gene index for cattle
                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pec
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                    mRNA sequence.
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                                                LeuTyrAlaPheValGlyValLysPheArgGluArgMetTrpMetLeuLeuLeuArgLeu
                                                                                                                                                                                 Genome Res. 11 (4), 626-630 (2001)
21180013
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
                                                                                                                                              AspValAlaLysSerValThrSerGlyLeuGlyTyrMetHisCysCysLeuAsnProLeu
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                                   GGCTGCCCTGACCAGAGGTGCCACCAGCGGCAGCCATCAGCTTCC
                                                                                   CTCTATGCCTTTGTGGGTGTCAAGTTCCGAGAGCGGATGTGGGTGCTACTCGTGCGTCTG
                                                                                                                                  GACATAGCCAAGTCGGTCACGTCGGGCATGGGCTACATGCACTGCTGCCTCAACCCACTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BACKWARD: GTTTTCCCAGTCACGACG
Plate: 86 row: D column: 24
Seq primer: ATTTAGGTGACACTATAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 and -minmatch 12 options.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="MARC 1BOV"
/tissue_type="pooled"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           fat,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Vector: pCMV SPORT6; Site_1: xbaI; Site_2: xhoI;
Library made from pooled tissue from lymph node, ovary,
fat, hypothalamus, and pituitary."
152 c 148 g 99 t
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JOURNAL COMMENT
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Identification of expressed genes from Japanese fle
(Paralichthys olivaceus) leukocytes stimulated with
Unpublished (2000)
Contact: Ikuo Hirono
Laboratory of Genetics and Biochemistry
Tokyo University of Fisheries
Konan 4-5-7, Minato-ku, Tokyo 108, Japan
Email: hirono@tokyo-u-fish.ac.jp.
                                                                                                                               LeuThrLeuProLeuTrpAlaValAspAlaAlaValGlnTrpValPheGlySerGlyLeu
                                                                                                                                                                CTCCTGCGCATCACTGAGATATACCTACTTCACCTCGCCCTGGCCTGACCTCATGCTCCTT
                                                                                                                                                                                                                                                              PheLeuLeuGlyLeuLeuGlyAsnGlyAlaValAlaAlaValLeuLeuSerArgArgThr
CysIleSerPheAspArgTyrLeuAsnIleValHisAlaThrGlnLeuTyrArgArgGly
                                                                                                                                                                                                                                TGCAAGCTGATGGGCCTGATGAAACATCTCAATCTCCTCTGTGGGAGTTTCCTTTTAGCT
                                                              CysLysValAlaGlyAlaLeuPheAsnIleAsnPheTyrAlaGlyAlaLeuLeuLeuAla
                                                                                                AlaLeuSerSerThrAspThrPheLeuLeuHisLeuAlaValAlaAspThrLeuLeuVal
                                                                                                                                                                                                                                                                                                  GAAGAGGAGCGCCTGCAGACCCTCGGCACTGTGTTCCAGCCTGTGTTGTACAGCTTGATC
                                                                                                                                                                                                                                                                                                                                                                                                   CysProGlnAspPheSer-----
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                                                                                                                                                                                                                                                                                                                                 ------LeuAsnPheAspArgAlaPheLeuProAlaLeuTyrSerLeuLeu 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Paralichthys olivaceus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Reukaryota; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes; Pleuronectoidei; Paralichthyidae; Paralichthys.

1 (bases 1 to 971)
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/clone_lib="lambda ZAPII-Con
/cell_type="leukocytes"
/dev_stage="adult"
/dev_stage="adult" 297 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Paralichthys olivaceus"
/db_xref="taxon:8255"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AspValAlaLysSerValThrSerGlyLeuGlyTyrMetHisCysCysLeuAsnProLeu 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CysGlnTyrAsnPheProGlnVal---GlyArgThrAlaLeu-----ArgValLeu 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LeuProAspPheIlePheLeuSerAlaHisHisAspGlu---ArgLeuAsnAlaThrHis 249
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mu
1 (bases 1 to 468)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                          Seq |
High
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468 bp mRNA linear EST 01-DEC--
maa56a05.yl Soares mouse 3NbMS Mus musculus cDNA clone
IMAGE:3820689 5' similar to TR:088410 088410 CHEMOKINE RECEPTOR
                                                                                                                                                                                                                                                                                                                                                      EST
                                                                                                                                                                                Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free
                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                          Unpublished (1997)
                                                                                                                                                                                                                                                                                                                         Mus musculus
                                                                                                                                                                                                                                                                                                                                                                    BF452722.1 GI:11518891
                                                                                                                                                       MGI:1457041
                                                                                                                                                                   IMAGE Consortium (info@image.llnl.gov)
                                                                                                                                                                                                                                                                                                                                         nouse mouse.
                                                                                                            primer: -40RP from Gibco h quality sequence stop: 382.
                                                                                                                                                                                                                                         Gene Index
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                                        /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:3820689"
               /sex="male"
                            /clone_lib="Soares mouse
/tissue_type="Spleen"
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v) for further
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                                                                                                                                                                                                           BE589641
195994 BA
            gland cDNA library
Unpublished (2000)
Contact: Sonstegard
                                                                                      Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Cetartioda Bovidae; Boviae; Bos. 1 (bases 1 to 511)
                                                                                                                                            Bos taurus
                                                                                                                                                                                 BE589641
BE589641.1
                                                Mapping
                                                                           Sonstegard, T.S., Capuco, A.V.,
                                                                Wells, K.D.
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/lab_host="DH10B"
Beltsville Agricultural
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Mismatches:
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Query Match:
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                                                                                                                                                   CTC -
                                                                                                                                                                                                 Leu
                                                                                                                                                                                                                                                                AlaValAspAlaAlaValGlnTrpValPheGlySerGlyLeuCysLysValAlaGlyAla 176
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                                                                                                                                                                                                                                          GCAGTGGATGCAGCCATCCAGTGGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCGGGTGCA
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Fax: 301 504 8414
Email: tads@lpsi.barc.usda.gov
Single pass sequencing. Bases ca
v0.980904.e. Vector identified b
  AK019478 3005 bp mRNA linear HTC Mus musculus 0 day neonate skin cDNA, RIKEN full-length library, clone:4632401H02:chemokine (C-C) receptor 10, f
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FORWARD: AGGAAACAGCTATGACCAT
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a 167 c 135 g 112 t
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/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Hazada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y., RIKEN integrated sequence analysis (RISA) system-384 format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
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AK019478
AK019478.1
Submitted (18-AUG-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
                                                                 cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group Genomic Sciences Center and Genome Science Laboratory in I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y., Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new (Genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                        URL:http://genome.gsc.riken.go.jp/,
Fax:81-45-503-9216)
                                                                                                                                          further details.
                                                                                                                                                             Please visit our web site (http://genome.gsc.riken.go.jp/)
                                                                                                                                                                                                                                                                                                                                                          Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 409, 685-690 (bases 1 to 3005)
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Meth. Enzymol. 303, 19-44 (1999)
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Mammalia; Eutheria;
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enriched mouse cDNA library
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US-09-101-518A-2 (1-415) x AK019478 (1-3005)
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Query Match:
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                                                                                          ArgThrAlaLeuSerSerThrAspThrPheLeuLeuHisLeuAlaValAlaAspThrLeu ::: |||||| |||||||||:::||||||| |||
TTTCTTGCCACTCTTCCCCTTCTGGGCCATTGCTGCTGCTGGTCAATGGATGTTCCAGACC
                                 LeuValLeuThrLeuProLeuTrpAlaValAspAlaAlaValGlnTrpValPheGlySer 168
                                                                         ACAAGAGTGAAGACCATGACTGACATGTTCCTTTTGAATTTAGCCATTGCTGATCTGCTC
                                                                                                                                                  CTTGTGTTCATTGTGGGCACCTTGGGCCAACAGCCTGGTCATCCTTGTCTACTGGTATTGC
                                                                                                                                                                                   LeuLeuPheLeuLeuGlyLeuLeuGlyAsnGlyAlaValAlaAlaValLeuLeuSerArg
                                                                                                                                                                                                                             ---TGTAAGAAAAATAATGTCAGGCAGTTTGCAAGCCATTTTCTTCCACCTCTGTACTGG
                                                                                                                                                                                                                                                                ProCysProGlnAspPheSerLeuAsnPheAspArgAlaPheLeuProAlaLeuTyrSer 108
                                                                                                                                                                                                                                                                                                            AATTTCAGTAGCTTCTTC-------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                814
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/dev_stage="0 day neonate"
296. .1405
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/db_xref="GI:12899710"
/tanslation="MMPTELTSLIPGMEDDESYDSTASTDDYMNLNESSFECKKNNVR
QFASHFLPPLYMLVFIVGTLGNSLVILVYWYCTRVKTMTDMFLLNLAIADLLFLATLP
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296. .
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RLLYSKMVCITIWVMAAVLCTPEILYSQVSGESGIATCTMVYPKDKNAKLKSAVLILK
VTLGEFLPFWYMAFCYTIIIHTLVQAKKSSKHKALKVTITVLTVFIMSQFPYNSILVV
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/note="putative"
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Roest-Crollius, H., Jaillon, O., Dasily Bouneau, L., Billault, A., Quetier, F., Weissenbach, J.
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TGTGAGCGATGATAGACTGAACCGAACAATGTGCTTTCGTAACTATTT-AATGTTCACGA
                          aHisHisAspGluArgLeuAsnAlaThrHisCysGlnTyrAsnPheProGlnVal-----
                                                      CATGGCTGCCTGGCTTTTCTCCCTACTGCTCTCCATTACAGACCTGGTCTTTCTAGAAGC
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Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases This sequence is a single read and was generated as part of scale clone-end sequencing project of the Tetracdon nigrov genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetracdon.
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/db_xref="taxon:99883"
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Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www
                                                                                                                                                                                                                                                                                                                                                                                                      Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished (2001)
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                          /note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life
Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : filang@lifetech.com URL :
http://fulllength.invitrogen.com"
261 c 232 g 250 t
                                                                                                                                                                                   /tissue_type="neuroblastoma cells"
/lab_host="DH10B"
                                                                                                                                                                                                                      /sex="male"
                                                                                                                                                                                                                                    /clone_lib="LTI_NFL001_NBC4"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM11865 row: 1 column: 13
High quality sequence stop: 835.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
I (bases 1 to 871)
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603300354F1 NIH_CGAP_Mam3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1999)
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National Institutes of Health, Mammalian
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                         Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and trimmed with phred
v0.980904 e. Vector identified by cross_match with the -min
                                                                   USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                    Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G. Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and Keele, J.W.
                                                                                                                                Contact: Smith TPL
                                                                                                                                                                     Sequence evaluation of four pooled-tissue normalized libraries and construction of a gene index for cattle
                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Cetartioda Bovidae; Bovinae; Bos
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36085 MARC 1BOV Bos taurus
AW354767 GI:6853757
                                                                                                                                                         Genome Res. 11 (4), 626-630 (2001)
                                                                                                                                                                                                                                                                                                                                  Bos taurus
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       PRimers
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Best Local Similarity:
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                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata
Mammalia; Eutheria; Primates
1 (bases 1 to 944)
Li,W.B., Gruber,C., Jessee,J
Full-length cDNA libraries a
Unpublished (201)
Contact: Genoscope
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AL523112 LTI_NFL003_NBC3 Homo
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 Genoscope - Centre
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primer: ATTTAGGTGACACTATAG.
Location/Qualifiers
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/tissue_type="pooled"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Bos taurus"
/db_xref="taxon:9913"
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466.00
80.00%
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National de
                                                                                 Chordata;
Primates;
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Sequencage
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ThrPheLeuLeuHisLeuAlaValAlaAspThrLeuLeuValLeuThrLeuProLeuTrp 156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Vector: pcMV SPORT6; Site_1: XbaI; Site_2: XhoI; Library made from pooled tissue from lymph node, ovary, fat, hypothalamus, and pituitary."

131 c 102 g 89 t
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and Polayes,D.
d normalization
                                                      Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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                                                                    euProLeuLeuValMetAlaTyrCysTyrAlaHisIleLeuAlaValLeuLeuValSerA 293
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GCCTCACGCAGACGGTGAAGGGGGGCGAGCGCCGTGGCSAGGGTGGCCCTGGGCTTCGCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGCAGGGGCTCTTCAGGGCTGGAGTCTGGGAAGTGCCACCTGCCGCACCATCTCTGGCCT 291
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                                                                                                                                                                                                           -GlnValGlyArgThrAlaLeuArgValLeuGlnLeuValAlaGlyPheLeuL 273
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a 357 c 301 g 174 t 6 others
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/lab_host="DH10B"
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                       CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLN
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information of
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMI1473 row: m column: 09
High quality sequence stop: 827.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mammalia; Eutheria; Primates; Cat
1 (bases 1 to 910)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Ma
Unpublished (199)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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603049139F1 NIH_MGC_116 Homo
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Tissue Procurement: Life Technologies, Inc.
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                                                             210
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                                                                                            PORTO-SPORTS; Site_1: NotI; Site_2: EcoRV (destroyed); RNA SOURCE anonymous pool of 3 colons, age 26 yo male, 49 yo female, 71 yo male colon; 46 yo male kidney, and pool of stomachs, 62 yo male and 70 yo female. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code
                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                   295 GlnArgArgLeuArgAlaMetArgLeuValValValValValAlalaPhe-AlaLeuCy 314
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533 AAGGTGGTCTATGTTGGCGTCTGGATCCCTGCCTGCTCATCTATTCCCGACTTCATC 592
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         59 GAACCAGCGGTTACCATGGAGGGGATCAGTATATACACTTCAGATAACTACACCGAGGAA 118
TIGGCTGCCTTACTACTTTGGGATCAGCATCGAATTCCTTTCACCTCCTGGA 878
                                               CACCAGAAGCGCCAGGCCCTCCAGACCACAGTCATCCTCATCCTGGCTTTCTTCGCCCTG
                                                                                           GETATTGTCATCCTGCTGCTATTGCATTATCATCTCCAAGCTGTCACACTCCAAGGGC
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-TRANS=human40.cdi -LIST=45 -DCCALIGN=200 -THR_SCORE-pct -THR_MX=100
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Minimum DB seq
Maximum DB seq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Post-processing: Minimum Match 0%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Searched:
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Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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length: 2000000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1891 1891 1891	1897 1897 1897 1897	2073 2073 1897 1897	2142 2142 2142 2136 2136	Score
87.9 87.9 87.9	888.2 88.2 2	96.4 96.4 88.2	99.6 99.6 8.4.8	Query Match
1107 1107 1107	1670 1670 1670 1670	1293 1293 1670 1670	1876 1876 1876 1877 6604	Length DB
15 15	325 36 4	14 36 14 24	15	BB B
US-09-170-496-19 US-09-170-496C-19 US-09-170-496D-19	US-09-633-541-1 US-09-663-702-1 US-09-663-799-1 US-09-880-107-3833	US-09-016-434-1052 US-09-960-706-962 US-09-023-655-980 US-09-624-594-1	PCT-US96-00499-1 PCT-US96-00499A-1 US-09-101-518-1 PCT-US00-26524B-2115 US-60-258-273-3	
	Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 3833, Ap	Sequence 1052, Ap Sequence 962, App Sequence 980, App Sequence 1, Appli	Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 2115, Ap Sequence 3, Appli	•

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PCT-US96-00499-1
                                          APPLICATION NUMBER: PCT/US96/
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
NAME: FEITATO, Gregory D
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 3258
TELECOMMUNICATION INFORMATION:
TELEPAN: 201-994-1740
TELEPAN: 201-994-1740
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1876 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application PC/TUS9600499
GENERAL INFORMATION:
APPLICANT: LI, Yi
TITLE OF INVENTION: HARTUGE
TITLE OF INVENTION: HARTUGE
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi, ADDRESSEE: Stewart & Olstein
STREET: 6 Becker Farm Road
CITY: Roseland
STATE: NJ
COUNTRY: USA
ZIP: 07068-1739
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
DESTINATION DATA:
DESTINATION DATA:
COURTED TO THE COUNTRY APPLICATION DATA:
COUNTRY APPLICATION DATA:
COUNTRY APPLICATION DATA:
COUNTRY APPLICATION DATA:
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  MOLECULE TYPE:
FEATURE:
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7 US-09-698-013-414
7 US-09-698-013-1151
7 US-10-029-386-17324
6 US-09-997-722-157
6 US-60-360-207-6145
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75 US-60-229-515-1889
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US-90-110-701C-21

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US-09-699-011A-485

US-60-213-159-650

US-60-213-170-650

US-60-213-170-650

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US-09-170-496D-173
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Sequence 159, Appl
Sequence 158, Appl
Sequence 188, Appl
Sequence 1889, Ap
Sequence 227, Appl
Sequence 2174, Appl
Sequence 8718, Appl
Sequence 8718, Appl
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ee 485, App
ee 650, App
ee 650, App
ee 650, App
ee 16, App
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ee 11311, Ap
ee 414, App
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                      CysTyrAlaHisIleLeuAlaValLeuLeuValSerArgGlyGlnArgArgLeuArgAla
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PCT-US96-00499A-1
    Percent Similarity:
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                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, V
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/00499
FILING DATE: 11 JAN 1996
CLASSIFICATION:
                                                                                                                                                                      TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1876 base pairs
                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33,073
REFERENCE/DOCKET NUMBER: 3258
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
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TITLE OF INVENTION: HUM:
TITLE OF INVENTION: HSA'
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
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STRANDEDNESS: single
TOPOLOGY: linear
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STREET: 6 Becker
CITY: Roseland
STATE: NJ
COUNTRY: USA
ZIP: 07068-1739
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APPLICANT: Li, Yi
ITITLE OF INVENTION: Human G-Protein Chemoki
FILLE REPERENCE: PP218PCT.US
CURRENT APPLICATION NUMBER: US/09/101,518
CURRENT FILING DATE: 1998-12-21
PRIOR APPLICATION NUMBER: PD7/US96/00499
PRIOR FILING DATE: 1996-01-11
PRIOR FILING DATE: 1996-01-11
SOFTWARE: PATENTION Ver. 2.1
SOFTWARE: PATENTIN Ver. 2.1
SOFTWARE: PATENTIN Ver. 2.1
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Pred. No.:
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LOCATION: (173)..(1420)
-09-101-518-1
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ORGANISM: HOMO
FEATURE:
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99.76%
99.76%
99.58%
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Matches:
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RESULT 4
PCT-US00-26524B-2115
PCT-US00-26524B-2115, Appl
Sequence 2115, Application PC/TUS002652
GENERAL INFORMATION:
APPLICANT: Birse et. al.
TITLE OF INVENTION: Colon and Colon Cal
FILE REFERENCE: PA005PCT
CURRENT APPLICATION NUMBER: PCT/US00/21
CURRENT FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: 60/157,137
PRIOR FILING DATE: 1999-09-9
PRIOR APPLICATION NUMBER: 60/163,280
PRIOR APPLICATION NUMBER: 60/163,280
PRIOR FILING DATE: 1999-11-03
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Best Local Similarity:
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; TYPE: DNA
; ORGANISM: Homo sapiens
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SOFTWARE: PatentIn Ver
SEQ ID NO 2115
LENGTH: 1877
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GENERAL INFORMATION:

APPLICANT: Beasley, Ellen
TITLE OF INVENTION: ISOLATED HUMAN NUCLEAR HORMONE RECEPTOR
TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUM.
TITLE OF INVENTION: HORMONE RECEPTOR PROTEINS, AND USES THEREOF
FILE REFERENCE: CL001042-PROV
CURRENT APPLICATION NUMBER: US/60/258,273
CURRENT FILING DATE: 2000-12-27
NUMBER OF SEQ ID NOS: 312
SOFTWARE: FRANSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 6604
TYPE: DNA
ORGANISM: Human
US-60-258-273-3
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Best Local Similarity:
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 1052, Application INFORMATION:
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; CLONE: g1002740
US-09-016-434-1052
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INFORMATION FOR SEQ ID NO: 1/
SEQUENCE CHARACTERISTICS:
LENGTH: 123 base pairs
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APPLICATION NUMBER:
FILING DATE:
CLASSLFICATION:
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 37,071
REGISTRATION NUMBER: PA-00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEPHONE: (650) 845-4466
                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
FILLING DATE: HEREWITH
CLASSIFICATION:
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APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
NUMBER OF SEQUENCES: 1490
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STREET: 3174 PORT
CITY: PALO ALTO
STATE: CALIFORNIZ
COUNTRY: USA
ZIP: 94304
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RESULT 7

US-09-960-706-962

Sequence 962, Application US/09960706

GENERAL INFORMATION:

APPLICANT: Munger, William E.

TITLE OF INVENTION: Identifying Drugs for and District OF INVENTION: Gene Expression Profiles

ITLE OF INVENTION: Gene Expression Profiles

FILE REFERENCE: 44921-5029-01US

CURRENT APPLICATION NUMBER: US/09/960,706

CURRENT FILING DATE: 2001-09-24

PRIOR APPLICATION NUMBER: 60/223,323

PRIOR APPLICATION NUMBER: 09/873,319
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; OTHER INFORMATION:
US-09-960-706-962
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NUMBER OF SEQ ID NOS: 1124
SOFTWARE: PATENTIN VET. 2.1
SEQ ID NO 962
LENGTH: 1293
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STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORD PERFECT 6.1 for Windows/MS-DOS
SOFTWARE: WORD PERFECT 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
FILING DATE: HEREWITH
CLASSIFICATION:
APPLICATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
REFERENCE/DOCKET NUMBER: PA-0001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 980, Application US/09023655 GENERAL INFORMATION:
                                                                                                                                        TELEFAX: (650) 845-416
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1670 base
TYPE: nucleic acid
STRANDEDNESS: sinc
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
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APPLICANT: Susan G. Stuart
APPLICANT: Susan G. Stuart
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1508
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erSerProPhe	88.19% Indels: 24 Gaps: 5) x US-09-624-594-1 (1-1670)	Pred. No.: 2.47e-168 Length: 1670 Score: 1897.00 Matches: 369 Percent Similarity: 97.63% Conservative: 1 Best Local Similarity: 97.36% Mismatches: 5	ATION: 6 594-1 Scores:	STRANDEDNES TOPOLOGY: FEATURE: NAME/KEY:	INFO	TE	ATTORNEY AGENT INFORMATION: NAME: Brook Esq., David E. REGISTRATION NUMBER: 22,592		; COMPUTER: IBM PC compatible ; OPERATING SYSTEM: PC-DOS/MS-DOS ; SOFTWARE: Patentin Release #1.0, Version #1.30 ; CURRENT APPLICATION DATA:	g		TITLE OF INVENTION: IP-10/MIG RECEPTOR DESIGNATED CXCR3, TTTLE OF INVENTION: NUCLEIC ACIDS, AND METHODS OF USES THEREFOR NUMBER OF SEQUENCES: 4 CORRESPONDENCE ADDRESS:	ICE 1, APP RAL INFORM PLICANT:	Db 1116 TCTTCCCGCCGGGATTCATCCTGGTCTGAGACCTCAGAGGCCTCCTACTCGGGCTTG 1172 RESULT 9 NS-A9-524-594-1	1056 397	377 TrpMetLeuLeuLeuArgLeuGlyCysProAsnGlnArgGlyLeuGlnArgGlnProSer	Qy 357 HisCysCysLeuAsnProLeuLeuTyrAlaPheValGlyValLysPheArgGluArgMet 376	Qy 337 CysGlyArgGluSerArgValAspValAlaLysSerValThrSerGlyLeuGlyTyrMet 356
Qy 397 Serse	Qy 377 TrpMe Db 1056 TGGA	Qy 357 Hiscy: Db 996 CACTG	Qy 337 Cysg:	Qy 317 ProTy Db 876 CCCTV	Qy 297 ArgLe Db 816 CGCC	Qy 277 Valme Db 756 GTCA	Qy 257 ValG Db 696 GTGG	Qy 237 Leuse Db 636 CTGT	Qy 217 LeuT Db 576 CTCA	Qy 197 TyrLd Db 516 TACC	Qy 177 Leupl Db 456 CTCT	Qy 157 AlaV Db 396 GCAG	Qy 137 ThrPl Db 336 ACCT	Qy 117 GlyA: Db 276 GGCA		156	Db 96 GTGC' Qy 77 GlyG	Db 36 ACACO
SerSerArgArgAspSerSerTrpSerGluThrSerGluAlaSerTyrSerGlyLeu 415 	rpMetLeuLeuLeuArgLeuGlyCysProAsnGlnArgGlyLeuGlnArgGlnProSer 396 	ysCysLeuAsnProLeuLeuTyrAlaPheValGlyValLysPheArgGluArgMet 376 	ysGlyArgGluSerArgValAspValAlaLysSerValThrSerGlyLeuGlyTyrMet 356 	ProTyrHisLeuValValLeuValAspIleLeuMetAspLeuGlyAlaLeuAlaArgAsn 336 	rgLeuArgAlaMetArgLeuValValValValValValAlaPheAlaLeuCysTrpThr 316 	ValMetAlaTyrCysTyrAlaHisIleLeuAlaValLeuLeuValSerArgGlyGlnArg 296 	ValGlyArgThrAlaLeuArgValLeuGlnLeuValAlaGlyPheLeuLeuProLeuLeu 276 	LeuSerAlaHisHisAspGluArgLeuAsnAlaThrHisCysGlnTyrAsnPheProGln 256 	LeuThrCysLeuAlaValTrpGlyLeuCysLeuLeuPheAlaLeuProAspPheIlePhe 236 	TyrLeuAsnIleValHisAlaThrGlnLeuTyrArgArgGlyProProAlaArgValThr 216 	LeuPheasnIleasnPheTyrAlaGlyAlaLeuLeuLeuAlaCysIleSerPheAspArg 196 	AlaValAspAlaAlaValGlnTrpValPheGlySerGlyLeuCysLysValAlaGlyAla 176 	ThrPheLeuLeuHisLeuAlaValAlaAspThrLeuLeuValLeuThrLeuProLeuTrp 156):lyAsnGlyAlaValAlaAlaValLeuLeuSerArgArgThrAlaLeuSerSerThrAsp 136 	AsnPheAspArgAlaPheLeuProAlaLeuTyrSerLeuLeuPheLeuLeuGlyLeuLeu 116 		STGCTAAATGACGCCGAGGTTGCCGCCCTCCTGGAGAACTTCAGCTCTTCCTATGACTAT 155 SLyGluAsnGluSerAspSerCysCysThrSerProProCysProGlnAspPheSerLeu 96	ACACCACCCAGCAGCAGAGCACCAGCCAGCCATGGTCCTTGAGGTGAGTGA

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AMAE: BYOOK ESQ., David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: TK19
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1670 base pairs
TYPE: nucleic acid
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CITY: Lexington

STATE: MA

COUNTRY: USA

ZIP: 02173

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/633,541

FILING DATE:
CLASSIFICATION:
CLASSIFICATION:
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GENERAL INFORMATION:
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APPLICATION NUMBER:
FILING DATE:
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APPLICANT: Moser, Bernhard
TITLE OF INVENTION: IP-10/MIG RECEPTOR DESIGNATED CXCR3,
TITLE OF INVENTION: NUCLEIC ACIDS, AND METHODS OF USES THEREFOR
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CORRESPONDENCE ADDRESS:
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ER: TKI96-01
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CORRESPONDENCE ADDRESS: ADDRESSEE: Hamilton,
                  NUMBER OF SEQUENCES:
                                                                         APPLICANT:
                                     TITLE
                                                                                                                             TrpMetLeuLeuArgLeuGlyCysProAsnGlnArgGlyLeuGlnArgGlnProSer
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                                    INVENTION:
                                           Moser, Bernhard
Qin, Shixin
Mackay, Charles R.
                                                                       Loetscher, Marcel
                                     IP-10/MIG
                          ANTIBODIES,
                          RECEPTOR DESIGNATED CXCR3, NUCLEIC ACIDS, AND METH
                           METHODS
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Percent Similarity:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1670 base pairs
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 08/829,839
FILING DATE: <UNKNOWN>
ATTORNEY/AGENT INFORMATION:
NAME: Brook Esq., David E.
REGISTRATION NUMBER: 22,592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/663,702
FILING DATE: 15-Sep-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
                                                                                                    ThralaProSer------SerProPheProProSerGlnValSerAspHisGln
GCAGTGGACGCTGCCGTCCAGTGGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGTGCC
         AlaValAspAlaAlaValGlnTrpValPheGlySerGlyLeuCysLysValAlaGlyAla
                                                AACTTCGACCGGGCCTTCCTGCCAGCCCTCTACAGCCTCCTCTTTCTGCTGGGGCCTGCTG
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                                                                                                                                                                                                                           GlyGluAsnGluSerAspSerCysCysThrSerProProCysProGlnAspPheSerLeu 96
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CITY: Lexington
STATE: MA
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
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Matches:
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/663,799
FILING DATE: 15-Sep-2000
                                                                                                                                                      NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                        TITLE OF INVENTION:
                                                                                                                                                                                                           APPLICANT: Loetscher, Marcel
                                                                                                                                                                                                                                                                            HisCysCysLeuAsnProLeuLeuTyrAlaPheValGlyValLysPheArgGluArgMet 376
                                                                                                                                                                                                                                                                                                                                                                                                                       CysGlyArgGluSerArgValAspValAlaLysSerValThrSerGlyLeuGlyTyrMet 356
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                                                                                                  COUNTRY: USA
                                                                                                             STREET: Two Militia Drive CITY: Lexington STATE: MA
                                                                                                                                             ADDRESSEE: Hamilton,
                                                                                                                                                                                                  Moser,
                                                                                                                                                                            Bernhard
N: IP-10/MIG RECEPTOR
NUCLEIC ACIDS, AND
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SEQUENCE CHARACTERISTICS:
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR
                                        LeuThrCysLeuAlaValTrpGlyLeuCysLeuLeuPheAlaLeuProAspPheIlePhe|
                                                                                                                                                                                                                  GlyAsnGlyAlaValAlaAlaValLeuLeuSerArgArgThrAlaLeuSerSerThrAsp 136
                                                                                                                                                                                                                                                                                                               GlyGluAsnGluSerAspSerCysCysThrSerProProCysProGlnAspPheSerLeu
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CTCACCTGCCTGGCTGTCTGGGGGGCTCTGCCTGTTTTCGCCCCTCCCAGACTTCATCTTC
                                                                                                                              GCAGTGGACGCTGCCGTCCAGTGGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGTGCC
                                                                                                                                         AlaValAspAlaAlaValGlnTrpValPheGlySerGlyLeuCysLysValAlaGlyAla 176
                                                                                                                                                                       ThrPheLeuLeuHisLeuAlaValAlaAspThrLeuLeuValLeuThrLeuProLeuTrp
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R APPLICATION DATA:
APPLICATION NUMBER: 08/709,838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 1670 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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RESULT 13
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                          US-09-101-518A-2
                                                           Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                  APPLICANT: HOTCH, DATCH T.

APPLICANT: VOCKLEY, JOSEPH G.

APPLICANT: SCHERF, Uwe

APPLICANT: Gene LOGIC, INC.

TITLE OF INVENTION: Gene Expression Profiles in

FILE REFERENCE: 44921-5028 WO

CURRENT APPLICATION NUMBER: US/09/880,107

CURRENT FILING DATE: 2001-06-14

PRIOR APPLICATION NUMBER: US 60/231,379

PRIOR PILING DATE: 2000-06-14

PRIOR PILING DATE: 2000-01-02

NUMBER OF SEO ID NOS: 3950

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SEQ ID NO 3833
LENGTH: 1670
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GENERAL INFORMATION:
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TITLE OF INVENTION: Non-Endogenous, Constitu
TITLE OF INVENTION: Receptors
FILE REFERENCE: AREN-0040
CURRENT APPLICATION NUMBER: US/09/170,496
CURRENT FILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 286
SOFTWARE: Patentin version 3.0
SOFTWARE: Patentin version 3.0
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GENERAL INFORMATION:
APPLICANT: Behan, Dominic
APPLICANT: Chalmers, Derr
APPLICANT: Liaw, Chen W.
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APPLICANT: Behan, Dominic P.
APPLICANT: Chalmers, Derek T.
APPLICANT: Liaw, Chen W.
APPLICANT: Liaw, Chen W.
TITLE OF INVENTION: Non-Endogenous, Cons
TITLE OF INVENTION: Receptors
FILE REFERENCE: AREN-0040
CURRENT APPLICATION NUMBER: US/09/170,49
CURRENT FILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 286
SOFTWARE: Patentin version 3.0
SEQ ID NO 19
LENGTH: 1107
TYPE: DNA
ORGANISM: Homo sapiens
US-09-170-498C-19
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US-09-170-496C-19
Sequence 19, Application Us
GENERAL INFORMATION:
APPLICANT: Behan, Dominic
APPLICANT: Chalmers, Dere
APPLICANT: Liaw, Chen W.
TITLE OF INVENTION: Non-Es
TITLE OF INVENTION: Recei
FILE REFERENCE: AREN-0040
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-DB-Pending_Patents_NA_New -CFMT-fastap -SUFTX-P2n.rnpn -MINMATCH-0.1
-LOOPCL-0 -LOOPEXT-0 -UNITS-bits -START-1 -END--1 -MATRIX-blosum62
-TRANS-human40.cdi -LIST-45 -DCCALION-200 -THR_SCORE-pct -THR_MXX-100
-THR_MIN-0 -ALIGN=15 -MODE-LOCAL -OUTFMT-pto -NORM-ext -HEAPSIZE-500 -MINLEN-0
-MAXEEN-200000000 -USER-US09101518_@CGN_1_1_200_@runat_29102002_091057_29944
-NCPU-6 -ICPU-3 -NO_XLRXY -NO_MMAP -LARGEQUERY -NCEG_SCORES-0 -MAIT -LONGLOG
-DEV_TIMEOUT-120 -WARN_TIMEOUT-30 -THREADS-1 -XGAPOP-10 -XGAPEXT-0.5 -FGAPOP-6
-FGAPEXT-7 -YGAPOP-10 -YGAPEXT-0.5 -DELOP-6 -DELEXT-7
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//cgn2_6/ptodata/2/pna/PCT_NEW_COMB.seq!:*
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ALIGNMENTS

RESULT 1 US-09-101-518A-1

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                                                                                       AlaLeuArgValLeuGlnLeuValAlaGlyPheLeuLeuProLeuLeuValMetAlaTyr
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                            TGCTATGCCCACATCCTGGCCGTGCTGCTGCTTTCCAGGGGCCCAGCGGCGCCCTGCGGGCC
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Best Local Similarity:
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GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Colon and Colon Cancer A
FILE REFERENCE: PA005P1
CURRENT APPLICATION NUMBER: US/10/106,698
CURRENT FILING DATE: 2007-03-27
PRIOR APPLICATION NUMBER: US/10/26524
PRIOR FILING DATE: 2000-09-28
PRIOR FILING DATE: 1990-29
PRIOR APPLICATION NUMBER: US 60/157,137
PRIOR FILING DATE: 1990-129
PRIOR FILING DATE: 1999-11-03
NUMBER OF SEQ ID NOS: 8564
SOFTWARE: Patentin Ver. 3.0
SEQ ID NO 2125
LENGTH: 1877
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99.30%
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Sequence 962, Application
GENERAL INFORMATION:
APPLICANT: Gene Logic, I
APPLICANT: Munger, Will
APPLICANT: Kulkarni, P
APPLICANT: Kulkarni, P
APPLICANT: Gene Canada
APPLICANT: Waga, Iwao
APPLICANT: Yamamoto, JI
TITLE OF INVENTION: Gene
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                                                           962, Application
T: Waga, Iwao
T: Yamamoto, Jun
INVENTION: Identifying Drugs
INVENTION: Gene Expression
                         Gene Logic, Inc.
Munger, William E.
Kulkarni, Prakash
Getzenberg, Robert F
                                                           PC/TUS0230182
      Drugs
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Profiles
       Diagnosis
       of,
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CURRENT APPLICATION NUMBER: PCT/US02/30182
CURRENT FILING DATE: 2002-09-24
PRIOR APPLICATION NUMBER: 09/960,706
PRIOR FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 1124
SOFTWARE: PatentIN Ver. 2.1
SEQ ID NO 962
LENGTH: 1293
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
OTHER INFORMATION: Genbank Accession No. U2
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                FGCTTTTCGCCCTCCCAGACTTCATC
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255 660 600 215 540 195 480 420

360 135 300 240 95 180 75 120 55 60

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Sequence 620, Application PC/TUS0218947
(GENERAL INFORMATION:
APPLICANT: ROSetta Inpharmatics
TITLE OF INVENTION: Diagnosis and Prognosis c
FILE REFERENCE: 9301-175-228
CURRENT APPLICATION NUMBER: PCT/US02/18947
CURRENT FILING DATE: 2002-06-14
PRIOR APPLICATION NUMBER: 60/380,770
PRIOR APPLICATION NUMBER: 60/380,770
PRIOR APPLICATION SERVED FOR APPLICATION NUMBER: 60/380,770
PRIOR FILING DATE: 2002-05-14
NUMBER OF SEQ ID NOS: 2699
SEQ ID NO 620
                                                                                                                                                                                    ; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: NM_001504
DATABASE ENTRY DATE: 2001-06-18
PCT-US02-18947-620
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PCT-US02-18947-620
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TYPE: DNA
ORGANISM: Homo
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RESULT 5

PCT-US02-25766-2790

Sequence 2790, Application PC/
; GENERAL INFORMATION:
; APPLICANT: GENE LOGIC, INC.
; APPLICANT: MUNGER, William E
; APPLICANT: FAULK, Ronald
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APPLICANT: SUN, Hongwei
APPLICANT: WAGA, IWAG
APPLICANT: WAGA, IWAG
APPLICANT: WAGA, IWAG
APPLICANT: YAMAMOTO, Jun
TITLE OF INVENTION: Gene Expression Profiles in
FILE REFERENCE: 44921-5068-WO
CURRENT APPLICATION NUMBER: PCT/US02/25766
CURRENT FILING DATE: 2002-08-14
PRIOR APPLICATION NUMBER: US 60/311,837
PRIOR FILING DATE: 2001-08-14
NUMBER OF SEQ ID NOS: 13946
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2790
LENGTH: 1670
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
COTHER INFORMATION: Genbank Accession No. X95870
PCT-US02-25766-2790
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                                                       LeuThrCysLeuAlaValTrpGlyLeuCysLeuLeuPheAlaLeuProAspPheIlePhe
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CTGTCGGCCCACCACGACGACGCCTCAACGCCACCCACTGCCAATACAACTTCCCACAG
                                           CTCACCTGCCTGGCTGTCTGGGGGGCTCTGCCTGTTTTCGCCCTCCCAGACTTCATCTTC
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                                                                                                                                                                                                                                                                                                                   AACTTCGACCGGGCCTTCCTGCCAGCCCTCTACAGCCTCCTCTTTCTGCTGGGGCTGCTG
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APPLICANT: Roberts, Chris
APPLICANT: Van 't Veer, Laura
APPLICANT: Van de Vijver, Marc
APPLICANT: Bernards, Rene
APPLICANT: Bernards, Rene
FILE OF INVENTION: Diagnosis and Prognosis of
FILE REFERENCE: 9301-175-999
CURRENT APPLICATION NUMBER: US/10/172,118
CURRENT FILING DATE: 2002-06-14
PRIOR APPLICATION NUMBER: 60/380,770
PRIOR APPLICATION NUMBER: 50/380,770
PRIOR APPLICATION NUMBER: 50/380,770
                                                                                                                                                                                                                                                                                                APPLICANT: Dai, Hongy...

APPLICANT: He, Yudong

APPLICANT: Ho, Yudong

APPLICANT: Mao, Mao

APPLICANT: Roberts, Chris

APPLICANT: Van 't Veer, Laura

APPLICANT: Van de Vijver, Marc

APPLICANT: Tonnards, Rene
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                                US-09-101-518A-2 (1-415) x US-10-172-118-620 (1-1670)
                                                                Best Local Similarity:
Query Match:
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US-10-172-118-620
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US-10-172-118-620
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                                                                                       Percent Similarity:
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LENGTH: 1670
TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                                                                                      PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER:
DATABASE ENTRY DATE: 2001-0
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                                                         TrpMetLeuLeuLeuArgLeuGlyCysProAsnGlnArgGlyLeuGlnArgGlnProSer 396
                                                                                                      HisCysCysLeuAsnProLeuLeuTyrAlaPheValGlyValLysPheArgGluArgMet 376
                                                                                                                                                     CysGlyArgGluSerArgValAspValAlaLysSerValThrSerGlyLeuGlyTyrMet 356
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                                             TGGATGCTGCTCTTGCGCCTGGGCTGCCCCAACCAGAGAGGGCTCCAGAGGCAGCCATCG
                                                                                          CACTGCTGCCTCAACCCGCTGCTCTATGCCTTTGTAGGGGTCAAGTTCCGGGAGCGGATG
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Query Match:
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US-10-251-686-1
; Sequence 1, Application US/10251686
; GENERAL INFORMATION:
                                                                                                                                                                           US-09-101-518A-2 (1-415) x US-10-251-686-1 (1-1670)
                                                                                                                                                                                                                                                                 Score:
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                                                                                                                                                                                                                                                                                            Alignment
                                                                                                                                                                                                                                                   Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION: (617) 861-6240
TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                No.:
   156
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, B
STREET: Two Militia Dr
CITY: Lexington
STATE: MA
COUNTRY: USA
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                                                                                                                                                41 ThrAlaProSer-----
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APPLICATION NUMBER: US/08/829,839
FILING DATE: 31-MAR-1997
APPLICATION NUMBER: US 08/709,838
FILING DATE: 10-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                        SEQUENCE DESCRIPTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Brook Esq., David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE
ValLeuAsnAspAlaGluValAlaAlaLeuLeuGluAsnPheSerSerSerTyrAspTyr
                                                                                                                   GTGCTAAATGACGCCGAGGTTGCCGCCCTCCTGGAGAACTTCAGCTCTTCCTATGACTAT
                                                                                                                                                                                                                                                                                                                                                    NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/10/251,686 FILING DATE: 20-Sep-2002 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 1670 base pairs TYPE: nucleic acid STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
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Mackay, Charles
OF INVENTION: IP-10/N
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S, NUCLEIC ACIDS, AND METHODS OF USE THEREFOR
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RESULT 8
US-10-251-385-19
: Sequence 19, Application US/10251
: GENERAL INFORMATION:
: APPLICANT: Behan, Dominic P.
: APPLICANT: Chalmers, Derek T.
: APPLICANT: Liaw, Chen W.
: TITLE OF INVENTION: Non-Endogeno
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                                                                                                               HisCysCysLeuAsnProLeuTyrAlaPheValGlyValLysPheArgGluArgMet 376
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FITTLE OF INVENTION: Protein-Coupled TITLE OF INVENTION: Receptors FILE REFERENCE: AREN-0040 CURRENT APPLICATION NUMBER: US/10/251,385 CURRENT FILING DATE: 2002-09-20 PRIOR APPLICATION NUMBER: US/99/170,496 PRIOR FILING DATE: 1998-10-13 NUMBER OF SEQ ID NOS: 294 SOFTWARE: Patentin version 3.1 SEQ ID NO 19 LENGTH: 1107
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Best Local Similarity:
Query Match:
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Pred. No.:
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; ORGANISM: Homo
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Sequence 173, Application US/10251385
(GENERAL INFORMATION:
APPLICANT: Behan, Dominic P.
APPLICANT: Chalmers, Derek T.
APPLICANT: Chalmers, Derek T.
APPLICANT: Liaw, Chen W.
TITLE OF INVENTION: Non-Endogenous, Constitu
TITLE OF INVENTION: Protein-Coupled
TITLE OF INVENTION: Receptors
FILE REFERENCE: AREN-0040)
CURRENT APPLICATION NUMBER: US/10/251,385
CURRENT FILING DATE: 2002-09-20
PRIOR APPLICATION NUMBER: US/09/170,496
PRIOR APPLICATION NUMBER: US/09/10/251,385
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US-10-035-832-1409
; Sequence 1409, Application US/10035832
; GENERAL INFORMATION:
; APPLICANT: MOTRIS, David
; APPLICANT: Engelhard, Eric
; TITLE OF INVENTION: MOVEL COMPOSITIONS AN
; FILE REFERENCE: A-71249/RMS/DCF
; CURRENT APPLICATION NUMBER: US/10/035,832
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SEQ ID NO 1409
LENGTH: 34570
TYPE: DNA
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PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US 09/798,586
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 1613
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                                                                                                       22341
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LOCATION: (1)..(448)
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                                                                      TrpValPheGlySerGlyLeuCysLysValAlaGlyAlaLeuPheAsnIleAsnPheTyr 183
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GENERAL INFORMATION:

APPLICANT: MORIS, David

APPLICANT: Engelhard, Eric

TITLE OF INVENTION: MOVEL COMPOSITIONS AND ME
FILE REFERENCE: A-71249/RMS/DCF

CURRENT APPLICATION NUMBER: US/10/035,832

CURRENT FILING DATE: 2002-07-22

PRIOR APPLICATION NUMBER: US 09/747,377

PRIOR FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: US 09/798,586

PRIOR FILING DATE: 2001-03-02

NUMBER OF SEQ ID NOS: 1613

SOFTWARE: PatentIn version 3.1
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Best Local Similarity:
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LENGTH: 1125
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                                                                                                                                                                       ATCTTCCTAGATACACTGGAGAGGCTGAAGGCTGTGAATAGCAGCTGCGAGCTGAGTGGC
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PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US 09/798,586
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEO ID NOS: 1613
SOFTWARE: Patentin version 3.1
SEO ID NO 1410
LENGTH: 2517
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APPLICANT: Engelhard, Eric
APPLICANT: Engelhard, Eric
TITLE ONE OF CANCER
FILE REFERENCE: A-71249/RMS/DCF
CURRENT APPLICATION NUMBER: US/10/035,832
CURRENT FILING DATE: 2002-07-22
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AlaThrHisCysGlnTyrAsnPheProGlnValGlyArgThr----
                                 GCCTTACCGGAACTCCTCTTTGCCAAGGTTGGCCAACCTCATAACAACGACTCCTTA----
                                                            AlaLeuProAspPheIlePheLeuSerAla-----HisHisAspGluArgLeuAsn
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37 ProGlyLeuTyrThrAlaProSerSerProPheProProSerGlnValSerAspHis 55	YAlaAlaGlnSerLysSerGlnThrLysSe	/ Match: 29.64% Indels: 13 Gaps: 9-101-518A-2 (1-415) x US-10-252-157-227 (1-1777)	No.:	ORMATION: In -227 res:	; TYPE: DNA ; ORGANISM: Homo sapiens ; FEATURE: ; NAME/KBY: misc feature	ER OF SEQ ID NOS: 501 WARE: PERL Program D NO 227 GTH: 1777	CURRENT APPLICATION NUMBER: US/10/252,157 CURRENT FILING DATE: 2002-10-01 PRIOR APPLICATION NUMBER: 60/295,048 PRIOR FILING DATE: 2001-05-31	; APPLICANT: Faris, Mary ; APPLICANT: Pearson, Cecelia I. ; TITLE OF INVENTION: GENES EXPRESSED IN PROSTATE CANCER ; FILE REFERENCE: PA-0027-1 US	RESULT 13 US-10-252-157-227 ; Sequence 227, Application US/10252157 ; GENERAL INFORMATION:	Qy 402 SerSerTrpSerGluThrSerGluAlaSer 411	Qy 382 ArgLeuGlyCysProAsnGlnArgGlyLeuGlnArgGlnProSerSerArgArgAsp 401 :::	Qy 362 ProLeuLeuTyrAlaPheValGlyValLysPheArgGluArgMetTrpMetLeuLeu 381 :::	Qy 342 ArgValAspValAlaLysSerValThrSerGlyLeuGlyTyrMetHisCysCysLeuAsn 361 :::: ::::::	Qy 322 ValLeuValAspIleLeuMetAspLeuGlyAlaLeuAlaArgAsnCysGlyArgGluSer 341 ::: ::: ::: ::: Db 841 ATCTTCCTAGATACACTGGAGAGGCTGAAGGCTGTGAATAGCAGCTGCGAGCTGAGTGGC 900	Qy 302 ArgLeuValValValValValAlaPheAlaLeuCysTrpThrProTyrHisLeuVal 321 ::: :::::: :::	Qy 283 AlaHisIleLeuAlaValLeuLeuValSerArgGlyGlnArgArgLeuArgAlaMet 301 ::::::	Oy 263 ArgValLeuGlnLeuValAlaGlyPheLeuLeuProLeuLeuValMetAlaTyrCysTyr 282	Db 604CCACAGTGCACCTTCTCCCAGGAAAACGAAGCGGAAACTAGAGCCTGGTTCACCTCC 660
Qy	Дy	ДУ	Qy	Qy Db	Qy Db	Qy	Qy Db	Qy Db	Qy	Qy	Оy	Оу	Оу	Оу	Оу	Qy db	Qy	Db
376 MetTrpMetLeuLeuArgLeuGlyCysProAsnGlnArgGlyLeuGlnArgGlnPro 395 ::: :::	356 MetHisCysCysLeuAsnProLeuLeuTyrAlaPheValGlyValLysPheArgGluArg 375 :::	336 AsnCysGlyArgGluSerArgValAspValAlaLysSerValThrSerGlyLeuGlyTyr 355	316 ThrProTyrHisLeuValValLeuValAspIleLeuMetAspLeuGlyAlaLeuAlaArg 335	296 ArgArgLeuArgAlaMetArgLeuValValValValValValAlaPheAlaLeuCysTrp 315 :::::	276 LeuValMetAlaTyrCysTyrAlaHisIleLeuAlaValLeuLeuValSerArgGlyGln 295 ::: :::	259ArgThrAlaLeuArgValLeuGlnLeuValAlaGlyPheLeuLeuProLeu 275	242 AspGluArgLeuAsnAlaThrHisCysGlnTyrAsnPheProGlnValGly 258 :::::	222 ValTrpGlyLeuCysLeuLeuPheAlaLeuProAspPheIlePheLeuSerAlaHisHis 241 :::	211 ProProAlaArgValThrLeuThr	191 CysileSerPheAspArgTyrLeuAsnIleValHisAlaThrGlnLeuTyrArgArgGly 210	171 CyslysValalaGlyAlaLeuPheAsnIleAsnPheTyrAlaGlyAlaLeuLeuLeuAla 190 	151 LeuThrLeuProLeuTrpAlaValAspAlaAlaValGlnTrpValPheGlySerGlyLeu 170 11	131 AlaLeuSerSerThrAspThrPheLeuLeuHisLeuAlaValAlaAspThrLeuLeuVal 150 ::: ::: 647 GGCCGCTCCGTCACTGATGTCTACCTGCTGAACCTAGCCTTAGCCTACTCTTTGCC 706	111 PheLeuLeuGlyLeuGlyAsnGlyAlaValAlaAlaValLeuLeuSerArgArgThr 130 	91 ProGlnAspPheSerLeuAsnPheAspArgAlaPheLeuProAlaLeuTyrSerLeuLeu 110 ::: ::: ::: 530 GAACCAGAATCCCTGGAAATCAACAAGTATTTTGTGGTCATTATCTATGCCCTGGTA 586	71 SerSerSerTyrAspTyrGlyGluAsnGluSerAspSerCysCysThrSerProProCys 90 :::	56 GlnValLeuAsnAspAlaGluValAlaAlaLeuLeuGluAsnPhe	377CCAGCGACCCAGTCAGGATTTAAGTTTACCTCAAAAATGGAAGATTT 424

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US-10-251-385-65
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CURRENT FILING DATE: 2002-09-20
PRIOR APPLICATION NUMBER: US/09/170,496
PRIOR FILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 294
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TITLE OF INVENTION: Non-Endogenous, (
TITLE OF INVENTION: Protein-Coupled
TITLE OF INVENTION: Receptors
FILE REFERENCE: AREN-0040
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                                                                 US-09-101-518A-2 (1-415) x US-10-035-832-1414 (1-1119)
                                                                                                                 Query Match:
                                                                                                                                                                                                    Alignment Scores:
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                                                                                                                                   Best Local Similarity:
                                                                                                                                                  Percent Similarity:
                                                                                                                                                                                                                                                                                  SEQ ID NO 1414
LENGTH: 1119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1414, Application US/10035832 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: MOSTIS, DAVID
APPLICANT: Engelhard, Eric
TITLE OF INVENTION: NOVEL COMPOSITIONS AND
FILE REFERENCE: A-71249/RMS/DCF
                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 09/798,586
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 1613
                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/10/035,832
CURRENT FILING DATE: 2002-07-22
PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR FILING DATE: 2000-12-22
                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                 ORGANISM: Homo
                                                                                                                                                                                                                                                                      TYPE: DNA
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                  67 LeuGluAsnPheSerSerTyr------AspTyrGluAsnGluSerAsp---
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TTCCTCTGCTGACACCCTACCACATCGTCATCTTCCTGGACACCCTGGCGAGGCTGAAG 864
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                                                  PheArgGluArgMetTrpMetLeuLeuLeuArgLeuGlyCysProAsnGlnArgGlyLeu 391
                                                                                                                     AlaLeuAlaArgAsnCysGlyArgGluSerArgValAspValAlaLysSerValThrSer 351
                                                                                                                                             ---SerAlaHisHisAspGluArgLeuAsnAlaThrHisCysGlnTyrAsnPheProGln 256
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TGCCAGCTCTTCCCTAGCTGGCGCAGG---AGCAGTCTCTCTGAGTCAGAGAATGCCACC 110:
                                   TTCCGCAGTGACCTGTCGCGGCTCCTGACGAAGCTGGGCTGTACCGGCCCTGCCTCCCTG 104
                                                                                                         GCCGTGGACAATACCTGCAAGCTGAATGGCTCTCTCCCCGTGGCCATCACCATGTGTGAG 924
                                                                                                                                                                                                    SerArgGlyGlnArgArgLeuArgAlaMetArgLeuValValValValValValAlaPhe 311
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Search completed: November Job time: 431 secs

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Result
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Perfect score:
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        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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2: /cgn2_6/ptodata/1,

3: /cgn2_6/ptodata/1,

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Listing first 45 summaries
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US-08-829-839-1
US-08-202-056-5
US-08-076-093A-5
US-08-08-701-265-5
US-08-801-265-8
US-08-801-228-5
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US-08-153-848-18
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8084.359 Million cell updates/sec
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RESULT US-08-7- Seque; Seque; Paten; GENE; App; April TI' TI' NUU; COU		22 22 23 23 23 24 24 24 24 25 26 26 27 27 28 28 28 28 28 28 28 28 28 28 28 28 28
RESULT 1 US-08-709-838-1 US-08-709-838-1 US-08-709-838-1 GENERAL INFORMATION: APPLICANT: LOETSCHET, APPLICANT: MOSET, BEIN TITLE OF INVENTION: IF TITLE OF INVENTION: IN UNMBER OF SEQUENCES: 4 CORRESPONDENCE ADDRESS: ADDRESSEE: Hamilton, STREET: Two Militia		216.6 216.6 211.8
Application US/08709838 5140064 CORMATION: SI LOSESCHER, Marcel SI MOSET, Bernhard SINVENTION: IP-10/MIG R INVENTION: NUCLEIC ACI P SEQUENCES: 4 UDENCE ADDRESS: SEE: Hamilton, Brook, SI Two Militia Drive		111.55 111.55 111.35 11
lication US/08709 064 ATION: LoetScher, Marcel Moser, Bernhard ENTION: IP-10/MI ENTION: NUCLEIC QUENCES: 4 CE ADDRESS: Hamilton, Brook wo Militia Drive		2160 2160 2160 2154 2154 2154 2154 2154 2154 2150 11510 1166 1106 1106 2517 2751 2751
ECEPTOR DESIGNATED DS, AND METHODS OF mith & Reynolds, P.	ALIGNMENTS	3 US-09-299-843A-14 US-09-088-3378-14 S PCT-US3)-11153-11 US-08-383-751A-1 US-08-383-751A-1 US-08-352-6781 S PCT-US93-09636-1 US-08-202-056-8 US-08-202-056-8 US-08-202-056-8 US-09-299-843A-65 US-09-299-843A-65 US-09-299-843A-65 US-08-292-43-65 S PCT-US92-02977-5 S PCT-US92-03022-4 3 US-08-982-493-5 US-08-982-493-5 US-08-982-493-5 US-08-982-493-5 US-08-982-493-5 US-08-982-493-5 US-08-153-848-23 US-09-299-843A-23 US-09-088-3378-23 S PCT-US93-11153-23
CXCR3, USES THEREFOR		Sequence 14, Appl Sequence 14, Appl Sequence 17, Appl Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 4, Appli Sequence 65, Appli Sequence 65, Appli Sequence 65, Appli Sequence 23, Appli

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                                                                                                                 US-08-709-838-1
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NAME: Brook Esq., David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: TKI9:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1670 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
                                            Query Match
Best Local Similarity
Matches 1550; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: TWO...
CITY: Lexington
STATE: MA
COUNTRY: USA
7IP: 02173
7IP: 02173
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/709,838
FILING DATE:
CLASSIFICATION: 530
CLASSIFICATION: 530
                                                                                                                                                               FEATURE:
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303 CCTCCCCGTTCCCGCCCTCACAGGTGAGTGACCACCAAGTGCTAAATGACGCCGAGGTTG 362
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                                              Score 1541.6;
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FILLING DATE: 10-SEP-196
ATTORNEY/AGENT INFORMATION:
NAME: Brook Esq., David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: TKI9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
TELEPEAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application Patent No. 6184358
GENERAL INFORMATION:
                                                                                                                                                       ADDRESSEE: Hamilton, Brook, Smith & STREET: Two Militia Drive CITY: Lexington STATE: MA COUNTRY: USA ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk COMPUTER: IBM FC COMPATIBLE COMPUTER: IBM FC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Ve CURENT APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Loetscher, Marcel APPLICANT: Moser, Bernhard APPLICANT: Oln, Shixin APPLICANT: Mackay, Charles R. APPLICANT: Mackay, Charles R.
                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: IP-10/MIG RITITLE OF INVENTION: ANTIBODIES, NUMBER OF SEQUENCES: 4
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APPLICATION NUMBER: US
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31-MAR-1997
2N: 435
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Best Local Similarity
Matches 1550; Conserv
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LENGTH: 1670 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
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APPLICANT: Chuncharapai, Anan
APPLICANT: Hebert, Caroline
APPLICANT: Hebert, Caroline
APPLICANT: Lee, James
APPLICANT: Lee, James
TITLE OF INVENTION: Antibodies to H
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb fla
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
                                                                                                                                                       GENERAL INFORMATION:
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5530
TELEFAX: 415/952-9881
TELEX: 910/371-7168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             763
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       823 CACCTGCCTGGCTGTCTGGGGGGCTCTGCCTGCCTTTTCGCCCCTCCCAGACTTCATCTTCCT 882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 523 CAACGGCGCGGTGGCAGCCGTGCTGAGCCGGCGGACAGCCCTGAGCAGCACCGACAC 582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    463 CTTCGACCGGGCCTTCCTGCCAGCCCTCTACAGCCTCCTCTTTCTGCTGGGGCTGCTGGG 522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        572 CAACGTCCTGGTGCTGGTGATCCTGGAGCGGCACCGGCAGACACGCAGTTCCACGGAGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       512 CTTCAAGGCCGTGTTCGTGCCCGTGGCCTACAGCCTCATCTTCCTCCTGGGCGTGATCGG 571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: single
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REFERENCE/DOCKET NUMBER: 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 07/677211 FILING DATE: 29-MAR-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
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                       TGCCCTCTGCTGGACCCCCTATCACCTGGTGGTGCTGGTGGACATCCTCATGGACCTGGG 1164
                                                                     CCAGCGGCGCCCTCAGCGGCAGAAGGCAGTCAGGGTGGCCATCCTGGTGACAAGCATCTT
                                                                                                                   TTCCAGGGGCCAGCGGCCTGCGGGCCATGCGGCTGGTGGTGGTGGTGGTGGCCTT 1104
                                                                                                                                                                                                                                                                        CCAAGCAGAAACGCATGCCTGGTTCACCTCCCGATTCCTTACCATGTGGCGGGATTCCT
                                                                                                                                                                                                                                                                                                                      GTCGGCCCACCACGACGACGCCTCAACGC-----CACCCACTGCCAATACAA 930
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                                                                                                                                                                      GCTGCCCATGCTGATGGGCTGGTGCTACGTGGGGTAGTGCACAGGTTGCGCCAGGC
                                                                                                                                                                                                                     GCTGCCCCTGCTGGTCATGGCCTACTGCTATGCCCACATCCTGGCCGTGCTG----CTGGT 1044
                                                                                                                                                                                                                                                                                                                                                                       CAAAGTCAGCCAAGGCCATCACAACAACTCCCTGCCACGTTGCACCTTCTCCCAAGAGAA
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1679 bases
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ilarity 57.0%;
Conservative
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25-FEB-1994
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GENERAL INFORMATION:
                                                                       Best Local Similarity Matches 507; Conserv
                                                                                                                Query Match
                                                                                                                                                                                                                                                           TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
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APPLICANT:
                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 70
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/255-530
TELEPHAX: 415/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 07/810782
FILING DATE: 19-DEC-1991
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 07/6
FILING DATE: 29-MAR-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 530 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: WinPatin (Ge
CURRENT APPLICATION DATA:
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                 463 CTTCGACCGGGCCTTCCTGCCAGCCCTCTACAGCCTCCTCTTTCTGCTGGGGCTGCTGGG 522
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
512 CTTCAAGGCCGTGTTCGTGCCCGTGGCCTACAGCCTCATCTTCCTCCTGGGCGTGATCGG 571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 460 Point San Brui
CITY: South San Francisco
                                                                                                                                                                                      TYPE: Nuclei
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                          NAME: Love, Richard REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/076,093A FILING DATE: 11-Jun-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                      TOPOLOGY:
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                                                                                                                                                                                    Nucleic Acid
EDNESS: Single
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                                                                           Conservative
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                                                                                                                                                                      Linear
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57.0%;
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                                                                         0; Mismatches
                                                                                         Score 240; DB 1;
Pred. No. 2.5e-42;
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US-08-701-265-5
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Patent No. 5776457
GENERAL INFORMATION:
                                                                                         APPLICANT: Chuncharapai, Anan APPLICANT: Lee, James APPLICANT: Hebert, Caroline APPLICANT: Jin Kim, K. TITLE OF INVENTION: Antibodies to NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
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ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                      GTTCCGCAGTGACCTGTCGCGGCTCCTGACGAAGCTGGGCTGTACCGGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAAAGTCAGCCAAGGCCATCACAACAACTCCCTGCCACGTTGCACCTTCTCCCAAGAGAA
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TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 1679 nucleotide:
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Best Local Similarity 57.0%;
Matches 507; Conservative
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APPLICATION NUMBER: 08/076093
FILING DATE: 11-Jun-1993
APPLICATION NUMBER: 07/810782
FILING DATE: 19-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/677211
APPLICATION NUMBER: 07/677211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 700
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5530
TELEPAX: 415/952-9881
TELEPAX: 415/952-9881
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
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ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B
REGISTRATION NUMBER: 34,6
                                                                                                                                                                                                                                                      812
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TYPE: Nucleic Acid
STRANDEDNESS: Single
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                                                                                                      GTCGGCCCACCACGAGCGCCCTCAACGC-------CACCCACTGCCAATACAA
                                                                                                                                                                 CACCTGCCTGGCTGTCTGGGGGGCTCTGCCTGCTTTTCGCCCTCCCAGACTTCATCTTCCT 882
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CCAAGCAGAAACGCATGCCTGGTTCACCTCCCGATTCCTTACCATGTGGCGGGATTCCT
                                     CAPAGTCAGCCAAGGCCATCACAACAACTCCCTGCCACGTTGCACCTTCTCCCAAGAGAA
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29-MAR-1991
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Pred. No. 2.5e-42;
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Patent No. 5840856
GENERAL INFORMATION:
APPLICANT: Chuntharapai, Anan
APPLICANT: Lee, James
APPLICANT: Hebert, Caroline
                                  INFORMATION FOR SEQ ID NO:
                                                                              NAME: Love, Richard B
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: 70
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5530
                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Jin Kim, K.
TITLE OF INVENTION: Antibodies
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
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                 SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: US/08/076,093A
FILING DATE: 11-Jun-1993
APPLICATION NUMBER: 07/810782
FILING DATE: 19-DEC-1991
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
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NAME: Love, Richard B
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                                          TELEPHONE: 415/225-55.
TELEFAX: 415/952-9881
TELEX: 910/371-7168
                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 460 Point San Bruno
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
LENGTH:
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                                                                                                                                                                                              APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
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                            GTTCCGGGAGCGGATGTGGATGCTCCTCTTGCGCCTGGGCTGCCCCAACC 1334
                                                                      AGGCCTGGGCTACATGCACTGCTGCCTCAACCCGCTGCTCTATGCCCTTTGTAGGGGTCAA 1284
                                                                                                                                    CGCTTTGGCCCGCAACTGTGGCCGAGAAAGCCAGGGTAGACGTGGCCAAGTCGGTCACCTC
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GTTCCGCAGTGACCTGTCGCGGCTCCTGACGAAGCTGGGCTGTACCGGCC
                                                         GTTCCTGGGCCTGGCCTGCTGCTCAACCCCATGCTCTACACTTTCGCCGGCGTGAA
                                                                                                                 GGCCGTGGACAATACCTGCAAGCTGAATGGCTCTCTCCCCCGTGGCCATCACCATGTGTGA
                                                                                                                                                                            CTTCCTCTGCTGGTCACCCTACCACATCGTCATCTTCCTGGACACCCTGGCGAGGCTGAA
                                                                                                                                                                                                         TGCCCTCTGCTGGACCCCCTATCACCTGGTGGTGCTGGACATCCTCATGGACCTGGG
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Pred. No. 2.5e-42;
0; Mismatches 365;
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US-08-805-478-5

Sequence 5, Applic Patent No. 5874543

Application US/08805478

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CLASSIFICATION DATA:

APPLICATION NUMBER: 08/284586
FILING DATE: 10-AUG-1994
PRIOR APPLICATION NUMBER: 08/076093
FILING DATE: 11-JUN-1993
PRIOR APPLICATION NUMBER: 07/810782
FILING DATE: 11-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: LOVE, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: 90706P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/25-5530
TELEFAX: 415/952-9881
TELEFAX: 415/952-9881
TELEFAX: 1679 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TROPOLOGY: Linear
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Best Local Similarity 57.0%;
Matches 507; Conservative
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APPLICANT: Chuntharapai, Anan
APPLICANT: Chuntharapai, Anan
APPLICANT: Hebert, Caroline
APPLICANT: Hebert, Caroline
APPLICANT: Jin Kim, K.
TITLE OF INVENTION: ANTIBODIES TO PF4A RECEPTOR
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
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OPERATING SYSTEM: PC-D
SOFTWARE: WinPatin (Ge
CURRENT APPLICATION DATA:
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STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
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CCTGAACATAGTTCATGCCACCCAGCTCTACCGCCGGGGCCCCCGGGCCCGGGGGCCCTGACCCT 822
                                          GCACAAAGTCAACTTCTACTGCAGCAGCCTGCTCCTGGCCTGCATCGCCGTGGACCGCTA 811
                                                                                  CTTCAACATCAACTTCTACGCAGGAGCCCTCCTGCTGGCCTGCATCAGCTTTGACCGCTA 762
                                                                                                                                                     AGTGGACGCTGCCGTCCAGTGGGGTCTTTTGGCCTCTGGCCTCTGCAAAGTGGCAGGTGCCCT 702
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                                                                                                                             GGCCGAGGGCTCTGTGGGCTGGGGTCCTGGGGACCTTCCTCTGCAAAACTGTGATTGCCCT 751
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 240; DB 2; Length 1679; Pred. No. 2.5e-42;
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RESULT 8
US-08-802-627A-5
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                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIIM TYPE: 3.5 inch, 1.44 mb floppy di
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/802,627A
FILING DATE: 19-Feb-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/284
FILING DATE: 10-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/076
FILING DATE: 11-JUN-1993
PRIOR APPLICATION NUMBER: 07/810
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APPLICANT: Wood, William I.
TITLE OF INVENTION: NUCLEIC ACID ENCODING PF4A RECEPTOR
NUMBER OF SEQUENCES: 6
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STREET: 460 Point San Bru
CITY: South San Francisco
                                                                                                                                                                                                                                                                                                                                                                ZIP: 94080
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    07/810782
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Matches
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: PO
TELECOMMUNICATION: INFORMATION:
TELEPHONE: 415/225-5530
TELEFAX: 415/952-9881
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 57.0 es 507; Conservative
                                                                                    TGCCCTCTGCTGGACCCCCTATCACCTGGTGGTGGTGGTGGACATCCTCATGGACCTGGG 1164
                              CGCTTTGGCCCGCAACTGTGGCCGAGAAAGCAGGGTAGACGTGGCCAAGTCGGTCACCTC
                                                                                                                                    CCAGCGGCGCCCTCAGCGGCAGAAGGCAGTCAGGGTGGCCATCCTGGTGACAAGCATCTT
                                                                                                                                                                 TTCCAGGGGCCAGCGGCCTGCGGGCCATGCGGCTGGTGGTGGTCGTGGTCGTGGCCTT 1104
                                                                                                                                                                                                                          GCTGCCCCTGCTGGTCATGGCCTACTGCTATGCCCCACATCCTGGCCCGTGCTG----CTGGT 1044
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GGCCGTGGACAATACCTGCAAGCTGAATGGCTCTCTCCCCGTGGCCATCACCATGTGTGA 1291
                                                                  CTTCCTCTGCTGGTCACCCTACCACATCGTCATCTTCCTGGACACCCTGGCGAGGCTGAA
                                                                                                                                                                                                      GCTGCCCATGCTGGTGATGGGCTGGTGCTACGTGGGGGTAGTGCACAGGTTGCGCCAGGC 1111
                                                                                                                                                                                                                                                                          CCAAGCAGAAACGCATGCCTGGTTCACCTCCCGATTCCTTACCATGTGGCGGGATTCCT
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Pred. No. 2.5e-42;
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US-08-801-238-5
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                                                                                                                                                                                                     Best Local Similarity
Matches 507; Conserv
                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WINPATIN (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/801,238
FILING DATE: 19-Feb-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 08/284
FRIGH ADTE: 10-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/076
FILING DATE: 11-UN-1993
PRIOR APPLICATION UMBER: 07/810
APPLICATION NUMBER: 07/810
FILING DATE: 19-DEC-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
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APPLICANT: Wood, William
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: PF4A RECEPTOR NUMBER OF SEQUENCES: 6
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ZIP: 940
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TOPOLOGY: Li
                                                                                                                                                                                                                                                                                                                                  TYPE:
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TELEFAX: 415/952-9881
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COMPUTER: IE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
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CTTCCTGCTCCACCTAGCTGTAGCAGACACGCTGCTGGTGCTGACACTGCCGCTCTGGGC
                                                                                         CAACGCCGCGGTGGCAGCCGTGCTGCTGAGCCGGCGGACAGCCCTGAGCAGCACCGACAC 582
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                                                       CAACGTCCTGGTGCTGGTGATCCTGGAGCGGCACCGGCAGACACGCAGTTCCACGGAGAC
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DEDNESS: Single
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Pred. No. 2.5e-42;
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                                                                                                                                                                                                                                                                                 Sequence 5, Application US/08801228 Patent No. 5922541 GENERAL INFORMATION:
                                                                                                                                                          APPLICANT: Lee, James
APPLICANT: WOOD, WILLIAM I.
APPLICANT: WOOD, WILLIAM I.
TITLE OF INVENTION: METHODS FOR DETECTION AND AMPLIFICATION
TITLE OF INVENTION: PF4A RECEPTOR NUCLEIC ACID
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 mb floppy
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
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                                                                                                STREET: 460 Point San Bruno
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                  ZIP: 94080
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Best Local Similarity 57.0%;
Matches 507; Conservative
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TELEPAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
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NAME: LOVE, RICHARD B.
REGISTRATION NUMBER: 90
REFERENCE/DOCKET NUMBER: 90
TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER: 08/0
FILING DATE: 11-JUN-1993
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APPLICATION NUMBER: 08/284586
FILING DATE: 10-AUG-1994
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APPLICATION NUMBER: US,
FILING DATE: 19-Feb-19
CLASSIFICATION: 435
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STRANDEDNESS: Single
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                GCTGCCCCTGCTGGTCATGGCCTACTGCTATGCCCACATCCTTGGCCGTGCTG----CTGGT 1044
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                                                                              CTTCCCACA---GGTGGGCCGCACGGCTCTGCGGGTGCTGCAGCTGGCTGTTTCT
                                                                                                                         CAAAGTCAGCCAAGGCCATCACAACAACTCCCTGCCACGTTGCACCTTCTCCCAAGAGAA
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GCTGCCCATGCTGATGGGCTGGTGCTACGTGGGGGTAGTGCACAGGTTGCGCCAGGC
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Pred. No. 2.5e-42;
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TOPOLOGY:
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US-09-104-296-5
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                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/925-5530
TELEFAX: 415/952-9881
TELEFX: 910/371-7168
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1679 base pairs
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Patent No. 6087475
GENERAL INFORMATION:
                                                                                                                                                                                                                   APPLICATION NUMBER: 08/076093
FILING DATE: 11-JUN-1993
PRIOR APPLICATION DATA: 07/810782
APPLICATION NUMBER: 07/810782
FILING DATE: 19-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: LOVE, RICHARD B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P0706P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION NUMBER: US/09/104,296
APPLICATION NUMBER: US/09/104,296
                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 08/6
FILING DATE: 06-JUN-1996
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/70
FILING DATE: 22-AUG-1996
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: PF4A Receptors NUMBER OF SEQUENCES: 6 CORRESPONDENCE ADDRESS:
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CTTY: South San F
                                     TYPE: Nucleic Acid STRANDEDNESS: Sing
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CLASSIFICATION:
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Best Local Similarity 57.0%;
Matches 507; Conservative
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                               GTTCCGGGAGCGGATGTGGATGCTGCTCTTGCGCCTGGGCTGCCCCAACC
                                                                                AGGCCTGGGCTACATGCACTGCTCCACCCGCTGCTCTATGCCTTTGTAGGGGTCAA 1284
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Pred. No. 2.5e-42;
0; Mismatches 365
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PCT-US94-06380-3

Sequence 3, Application PC/TUS9406380 GENERAL INFORMATION:
APPLICANT: Chuntharapai, Anan APPLICANT: Lee, James APPLICANT: Hebert, Caroline

K. Jin Kim

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TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1679 bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 08/076093
FILING DATE: 11-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: LOVE, RICHARD B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: 706F
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5530
TELEPAX: 415/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: PC_DOS/MS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
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883 GTCGGCCCACCACGAGGGGCGCTCAACGC------
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Local Similarity 57.0%;
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                                                   CACCTGTGGGACCATCTGGCTGGTGGGCTTCCTTCCTTGCCTTGCCAGAGATTCTCTTCGC
                                                                                   CACCTGCCTGGCTGTCTGGGGGGCTCTGCCTGCCTTTTTCGCCCTCCCAGACTTCATCTTCCT 882
                                                                                                                                                                                                                      CTTCAACATCAACTTCTACGCAGGAGCCCTCCTGCTGGCCTGCATCAGCTTTGACCGCTA 762
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                                                                                                                     CCTGAACATAGTTCATGCCACCCAGCTCTACCGCCGGGGGGCCCCCGGGCCCGCGTGACCCT
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F: 460 Point San Bruno
South San Francisco
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Pred. No. 2.5e-42;
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RESULT 13
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                                                                                                             CLASSIFICATION: 435
ATTORNEY PAGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: UCSF-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 343-4341
TELEPAX: (650) 343-4342
INFORMATION FOR SEQ ID:NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 7, Application US/08982493 Patent No. 6110695
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Gunn, Michael D
APPLICANT: Williams, Lewis T
APPLICANT: Cyster, Jason G
TITLE OF INVENTION: Modulatir
TITLE OF INVENTION: Receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 75 DENISE DRIVE
                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 2818 base pairs
                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOTTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
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STREET: /5 LL...
CITY: HILLSBOROUGH
STATE: CALIFORNIA
TTEA
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MOLECULE TYPE:
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                  TOPOLOGY:
                                     TYPE: nucleic acid
STRANDEDNESS: doub
                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                            Version
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RESULT 14
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; LOCATION:
US-08-982-493-7
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Sequence 1, Application US/08628655 Patent No. 6232123
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Best Local Similarity
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Pred. No. 6.2e-42;
0; Mismatches 366;
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatibl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: MONOCLONAL ANTIBODIES AGAINST
TITLE OF INVENTION: LEUCOCYTE-SPECIFIC G PROTEIN-COUPLED
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & F-3-
STREFFF.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: COTUZZÍ, LAUTA A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 841
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CLASSIFICATION: 424
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: FastSEQ for Windows CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
468
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CITY: N
STATE:
                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: Coding LOCATION: 85...12 OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08 FILING DATE: 13-AUG-1996
                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH:
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             CTTCAACATCAACTTCTACGCAGGAGCCCTCCTGCTGCTGCATCAGCTTTGACCGCTA
GCACAAAGTCAACTTCTACTGCAGCAGCCTGCTCCTGGCCTGCATCGCCGTGGACCGCTA
                                                           GCCCGAGGCTCTGTGGGCTGCGTCCTCGCTGCAAACTGTGATTGCCCT
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                                                                                                                         CTTCCTGTTCCACCTGGCCGTGGCCGACCTCCTGCTGGTCTTCATCTTGCCCTTTGCCGT
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            PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/2
FILING DATE: 02-MAY-94
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/2
FILING DATE: 15-MAR-94
                                                                                                                                                                                             ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
SOFTWARE: WordPerfect (Version 5.0)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Repliqen Corporation
APPLICANT: the Trustees of Boston University
TITLE OF INVENTION: ANTIBODIES TO INTERLEUKIN-8 RECEPTORS AND
TITLE OF INVENTION: METHODS OF USE
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CORRESPONDENCE ADDRESS:
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                                                                                                                                          FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                             COUNTRY: U.S.A.
ZIP: 02110-2804
                                                                                                                                                                                 APPLICATION NUMBER:
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APPLICATION DATA
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TELEX: 200154
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 04
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEPHONE: (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 07/6: FILING DATE: 10-APR-91 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 09-JUL-
PRIOR APPLICATION DATA:
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APPLICATION NUMBER:
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STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity les 491; Conserv
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                                  TTCCAGGCCCACATGGGGCAGAAGCACCGGGCCATGCGGGTCATCTTCGCCGTCGTGCTC
                                                                  CTGGTTTCCAGGGGCCAGCGCCCTGCGGGCCATGCGGCTGGTGGTGGTCGTTGGTG 1099
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                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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3: gb_ln:*
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Listing first 45 summaries
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                                     SUMMARIES
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L31584 Human G pro
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L24445 Oryctolagus
U19947 Bos taurus
AR016960 Homo sapi
AR003349 Sequence
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M82873 Oryctolagus
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AB003174 Mus muscu
AF045146 Mus muscu
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ALIGNMENTS

JOURNAL REFERENCE VERSION KEYWORDS REFERENCE SOURCE ACCESSION DEFINITION Locus ORGANISM TITLE AUTHORS JOURNAL AUTHORS 271144 bp DNA linear PRI 17-JUN-2001 Homo sapiens chromosome X sequence from 6 PACs 1 BAC and 1 cosmid, region GJB1-DXS559 map Xq13.1, complete sequence. AL590763 AJ239319
AL590763.1 GI:13751778 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 271144)

1 (bases 1, Heitmann, K., Sudbrak, R., Kosiura, A., Klages, S., Steffens, C., Borzym, K., Kube, M., Lehrack, S., Marquardt, I., Schuelzchen, S., Starke, A., Thompson, C., Hennig, S., Francis, F., Nemeth, A., Monaco, A., Lehrach, H. and Reinhardt, R. Direct Submission Submitted (15-FEB-1999) MPIMG, Abt.Lehrach, Max Planck Institut Fuer Molekulare Genetik, Ihnestrasse 73, Berlin, 14195 Germany MPIMG. Homo sapiens Unpublished human. (bases 1 to 271144)

Bases

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                                             TGTAGCAGACACGCTGCTGGTGCTGACACTGCCGCTCTGGGCAGTGGACGCTGCCGTCCA
                                                                                              CGTGCTGATGAGCCGGACAGCCCTGAGCAGCACCCGACACCTTCCTGCTCCACCTAGC
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33 a 59391 c 63906 g 76614 t
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1800 157561	QY 1741 AGCCACAGGCCCAGGCCTCCAGCTCAGCAGTGACTGTGGCCATGGTCCCCAAGACCTCTAT	
1740 157621	OY 1681 ACTTCATCTTCCCCAAGTGCGGGGAGTACAAGGCATGGCGTAGAGGGTGCTGCCCCATGA	
1680 157681	Qy 1621 CATCCTGCCGCCCGAGGTGGCTGCCTGGAGCCCCACTGCCCTTCTCATTTGGAAACTAAA 	
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1560 157801	OY 1501 CTCTCCCCAATATCCTCGCTCCCGGGACTCACTGGCAGCCCCAGCACCAGCACCAGGTCTCCC	
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1440 157921	OY 1381 CTGGTCTGAGACCTCAGAGGCCTCCTACTCGGGCTTGTGAGGCCGGAATCCGGGCTCCCCC	
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1140 158221	QY 1081 GGTGGTGGTGGTGGTGGCCTTTGCCCTCTGCTGGACCCCCTATCACCTGGTGGTGCT	
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1020 158341	QY 961 GGTGCTGCAGCTGGTGGCTGGCTGCTGCCCCCTGCTGGTCATGGCCTACTGCTATGC	
960 158401	OY 901 GCGCCTCAACGCCACCCACTGCCAATACAACTTCCCACAGGTGGGCCGCACGGCTCTGCG	
900 158461	QY 841 GGGCTCTGCTTTTTCGCCCTGCCAGACTTCATCTTCCTGTCGGCCCACCACGACGA	
840 158521	QY 781 CACCCAGCTCTACCGCCGGGGGCCCCGGGCCCGGGTGACCCTCACCTGCCTG	
780 158581	QY 721 CGCAGGAGCCCTCCTGCTGCCTGCATCAGCTTTGACCGCTACCTGAACATAGTTCATGC	

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Loetscher, M., Gerber, B., Loetscher, P., Jon Clark-Lewis, I., Baggiolini, M. and Moser, B. Chemokine receptor specific for IP10 and m and expression in activated T-lymphocytes J. Exp. Med. 184 (3), 963-969 (1996)
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X95876
X95876.1 GI:1552845
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1 (bases 1 to 1670)
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69. 1175
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Loetscher, M. and Moser, B.
Method of detecting or identifying
of CXC chemokine receptor 3
Patent: US 6140064-A 1 31-OCT-2000;
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Unclassified
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1 (bases 1 to 1563)
Gutierrez,J., Varona
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished
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//GD_XTG="SPTEMBL:015185"
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SPEPPSQVSDHQVLNDAEVAALLENFSSSYDYGENESDSCCTSPPCPQDESLNFDRAF
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Eutheria; Primates; Catarrhini; Hominidae;
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Pred. No. 1.2e-254;
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Score 1293; DB 9; Pred. No. 2.5e-222;

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U32674
U32674.1 GI:
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Marchese,A., Heiber,M., Nguyen,T.,
Cheng,R., Murphy,P.M., Tsui,L.-C.,
and Docherty,J.M.
                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (31-JUL-1995) B.F. O'Dowd,
                                                                                                                                                                                                                                                                                                                                                                                                                                       Cloning and chromosomal mapping of three novel genes, and GPR14, encoding receptors related to interleukin (neuropeptide Y, and somatostatin receptors Genomics 29 (2), 335-344 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and Docherty
Cloning and
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                                                                                                                                                                                                                                                                                                                                                 University of Toronto,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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1 (bases 1 to 1293)
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                                                       /product="GPR9"
/protein_id="AGC90505.1"
/protein_id="AGC90505.1"
/db_xref="GI:1002741"
/db_xref="GI:1002741"
/translation="VSDHQVLNDAEVAALLENFSSSYDYGENESDSCCTSPPCPQDFS
/translation="VSDHQVLNDAEVAAVLLSRFTALSSTDTPLHLAVADTLLVLTL
LNFDRAFLPALYSILFLIGHLGNGAVAAVLLSRFTALSSTDTPLHLAVATQLYRGP
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PARVTLTCLAVWGLCLLFALPDFIFLSAHHDERLNATHQQYNFPQVGFTALRVLQUVA
GFTLDLLVMAYCYHILAVLLVSRGQRRLRAMRLVVVVVVVAFALCWTPYHLVVLVDIL
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receptors"
                       PNQRGLQRQPSSSRRDSSWSETSEASYSGL"
458 c 357 g 277 t
                                                                                                                                                                                                           /gene="GPR9"
<109. .1203
                                              MDLGALARNCGRESRVDVAKSVTSGLGYMHCCLNPLLYAFVGVKFRERMWMLLLRLGC
                                                                                                                                                                                              <109. .1203
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                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="8"
/map="0p11.2-p12"
                                                                                                                                                                          /note="The initiating is an orphan receptor
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                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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Shi, X., Geor
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Shi, X., Georg
                                                                                                                                                                                                                                                                                                                                                Department of Pharmacology, k Rd., Toronto, Ontario M5S
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George,S.R., C
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Rattus norvegicus c
AF223642
AF223642.1 GI:8572
                                                                                                                                                                                                                                                                                 and Sarau, H.M.
Direct Submission
Submitted (11-JAN-2000)
Pharmaceuticals, Experin
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                                                                                                                                                                                                                                                                                                                                                              Mol. Phan
20286573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Norway rat.
Rattus norvegicus
Eukaryota; Metazoa;
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and Sarau, H.M.
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              Conservative
                                                                /translation="MYLEVSERQVLDASDIAFLLENSTSPYDYGENESDFSDSPPCPQ
DFSLNFDRTFLEVLYSTLFLLGLLGNAVAAVLLSQRTALSSTDTFLLHLAVADVLLV
LTLPLMAVDAAQMVESSGLCKVAGALFNINFYAGAFLLACISFDRYLSIVHATQIYR
RDPWYRVALTCIVVWGLCVLFALPDFIFLSASHDQRLNATHCQYNFPQVGRTALEVLQ
LVAGFLMPLLVMAYCVAHILAVLLVSRQQRRFRAMRLVVVVVVAFAVCWTPYHLVVLV
DILMGVGLARNCGRESHVDAKSVTSGMGYMHCCLNPLLYAFVGVKFKBQMWMLLMR
LGRSDQRGPQRQPSSBRRESSWSETTEASYLGL"

4 86 c 417 g 405 t
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149. .1
                                                                                                                                                  /product="chemokine ro/protein_id="AAF76982/db_xref="GI:8572057"
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                                                                                                                                                                                    /codon_start=1
                                                                                                                                                                                                                    /sex="male"
                                                                                                                                                                                                                             /organism="Rattus norvegicus"
/db_xref="taxon:10116"
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Experimental Station I
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Sciurognathi; Muridae;
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                    CGCAGCGGCAGCCTTCATCTTCACGGAGAGAATCATCCTGGTCTGAGACAACTGAGGCCT
                               TCCAGAGGCAGCCATCGTCTTCCCGCCGGGATTCATCCTGGTCTGAGACCTCAGAGGCCT
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Submitted (17-APR-1997) Masahiro Tamaru, Japan Tobacco Inc. Centra Submitted (17-APR-1997) Masahiro Tamaru, Japan Tobacco Inc. Centra Pharmaceutical Reseach Institute, Pharmaceutical Frontier Reseach Laboratories; 13-2, Fukuura 1-chome, Kanazawa-ku, Yokohama, Kanazawa 236, Japan (E-mail:tamaru@ikrl.jti.co.jp, Tel:81-45-786-7694, Fax:81-45-786-7692)
                                                                                                                                                                                                                                                                                                                                                           Mus musculus
Eukaryota; Metazoa; Chordata;
Eukaryota; Eutheria; Rodentia;
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99009219
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/db_xref="GI:3798732"
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Query Match
Best Local Similarity 76.0
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                                                                                                                                                                         Submitted (24-SEP-1999) Hitoshi Kato, University of Tokyo, Department of Human Genetics, Graduate School of Medicine; Hongo, Bunkyo-ku, Tokyo 113-0033, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                      319 bp
Homo sapiens gene for chemokine
AB032735
                                                                                                                                                                                                                   Kato, H., Tsuchiya, N. and Tokunaga, K. Direct Submission
                                                                                                                                                                                                                                                                                                         Single nucleotide polymorphisms in the coding CXC-chemokine receptors CXCR1, CXCR2 and CXCR3
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Mammalia; Eutheria; Primates;
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               /gene="CXCR3"
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                                                                                    /organism="Homo sapiens"
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                                                                                                                              ocation/Qualifiers
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                                                                                                                                               Submitted (24-SEP-1999) Hitoshi Kato, University of Tokyo, Department of Human Genetics, Graduate School of Medicine; Hongo, Bunkyo-ku, Tokyo 113-0033, Japan (E-mail:katoh@m.u-tokyo.ac.jp, Tel:81-3-5841-3693,
                                                                                                                                                                                                                                          Kato, H., Tsuchiya, N. and Tokunaga, K. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                          Kato,H., Tsuchiya,N. and Tokunaga,K. Single nucleotide polymorphisms in the coding regions CXC-chemokine receptors CXCR1, CXCR2 and CXCR3
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae
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/map="Xq13"
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AR015971
                                                                                          1 (bases 1 to 1679)
Lee, J. and Wood, W.I.
Antibodies to human PF4A receptor a
Patent: US 5776457-A 5 07-JUL-1998;
Location/Qualifiers
1. 1679
                                                                                                                                              Unclassified
                                                                                                                                                      Unknown
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GVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSSWSETSETSYSGL"
258
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Chuntharapai,A., Lee,J., Hebert,C. and Antibodies to a human PF4 superfamily Patent: US 5840856-A 5 24-NOV-1998;
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                                     CGCTTTGGCCCGCAACTGTGGCCGAGAAAGCAGGGTAGACGTGGCCAAGTCGGTCACCTC
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                      GGCCGTGGACAATACCTGCAAGCTGAATGGCTCTCTCCCCGTGGCCATCACCATGTGTGA
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Patent: US 5892017-A 5 06-APR-1999;
Location/Qualifiers
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                                                                                        CACCTGTGGGACCATCTGGCTGGTGGGCTTCCTTCCTTGCCAGAGATTCTCTTCGC
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TTCCAGGGGCCAGCGGCCTGCGGGCCATGCGGCTGGTGGTGGTCGTGGTGGCCTT
                      GCTGCCCATGCTGGTGATGGGCTGGTGCTACGTGGGGGTAGTGCACAGGTTGCGCCAGGC
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1 (bases 1 to 1679)
Lee, J. and Wood, W.I.
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                                                                                                   CACCTGCCTGGCTGTCTGGGGGGCTCTGCCTGCTTTTCGCCCTCCCAGACTTCATCTTTCCT 882
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                                                CACCTGTGGGACCATCTGGCTGGGCTTCCTTCCTTGCCAGAGATTCTCTTCGC
                                                                                                                                                     GCACAAAGTCAACTTCTACTGCAGCAGCCTGCTCCTGGCCTGCATCGCCGTGGACCGCTA
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Chuntharapai, A., Hebert, C., Kim, K.J. and Antibodies to human IL-8 type B receptor Patent: US 5440021-A 6 08-AUG-1995;
Location/Qualifiers
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         1285 GTTCCGGGAGCGGATGTGGATGCTGCTCTTGCGCCTGGGCTGCCCCAACC 1334
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Search completed: November 2, 2002, 06:06:32 Job time : 2828 secs

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Human G-protein ch
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Human ip-10/mig re
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DNA encoding human
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DNA encoding	ABK16594	24	1068	10.8	203.2	4.5
Human	AAA40128	17	1068	10.8		43
Human	ABL32812	24	6059	•	\circ	42
Human	AAS16876	24	12789		204.8	41
DNA	AAS77796	23	2785	10.9	204.8	40
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cDNA for	AAV25490	19	2154	•	•	37
DNA	AAV22684	19	2154	•		36
Epstein Barr	AAQ64125	15	2154	•	211.8	35
Human immune	AAK69854	22	2087		213.4	34
DNA encoding	AAA30729	21	1137		215	ω
DNA encoding	ABK16599	24	1068	11.5	216	32
Human	AAK69852	22	6923		216.6	31
Human	AAA91707	21	2160		216.6	30
Human V31 seven tr	AAV18347	19	2160		216.6	29
Putative	AAQ66160	15	2160		216.6	28
Genomic clone of	AAA90600	21	2058	11.5	216.6	27
Human V31 seven tr	AAV18345	19	2058	•	216.6	26
Putative	AAQ66153	15	2058		216.6	25
Human	AAA91709	21	1900	<u>, </u>	216.6	24
Human V31	AAV18349	19	1900	۲.	216.6	23
Partial coding seq	AAQ66162	15	1900	<u>. </u>	216.6	22
DNA encoding novel	AAS76560	23	1710		216.6	21
Human G protein-co	AAA30632	21	1137	۲.	216.6	20
Recombinant high a	AAQ99951	16	1373	Η.	217.8	19
DNA encoding nove	AAS83768	23	4017	2.	229	18
Human DNA sequence	AAS94899	24	3011	2	229	17
Recombinant high a	AAQ99949	16	1200		231	16
Sec	AAQ30011	13	1200	۲.	231	15
Human Burkitt lymp	ABA09117	22	3620	12.7	238.4	14
Human	AAX87710	20	2818	2	238.4	13
DNA encoding	AAA30727	21	1119	12.7	238.4	12
Human	AAA30626	21	11	12.7	238.4	11
Human	AAQ80522	16	1679	12.8	240	10

ALIGNMENTS

RESULT 1

primer_bind Key Homo signal transduction; gene therapy; diagnosis; ss. AAT72800; 11-JAN-1996; 11-JAN-1996; 17-JUL-1997. primer_bind Human G-protein chemokine receptor HSATU68 cDNA. 28-SEP-1997 AAT72800 standard; (HUMA-) HUMAN GENOME SCI INC WO9725340-A1 HSATU68; G-protein chemokine receptor; 7-transmembrane receptor; sapiens (first entry) complement (173..190) /*tag= b 1402..1420 /*tag= c 96WO-US00499. 96WO-US00499 Location/Qualifiers 173..1420 /*tag= CDNA; 1876 ΒP

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Matches
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                                                                                                                                                      TGCCGCCCTCCTGGAGAACCTTCAGCTCTTCCTATGACTATGGAGAAAACGAGAGTGACTC
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DB; AAW19780.
          GTGGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGTGCCCTCTTCAACATCAACTTCTA
                                                                                CGTGCTGAGCCGGCGGACAGCCCTGAGCAGCACCGACACCTTCCTGCTCCACCTAGC
                                                                                                            AGAAGCAGCCTTTGAGAAAGGGAAGTCACTATCCCAGAGCCCAGACTGAGCGGATGGAGTT
Similarity
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Pred. No. 0;
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Matches 1872
                                                                                                                                                                                                                           diagnosis and treatment of diseases associated with inappropriate P expression. For example, N and P may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of P by expressing inactive proteins or to supplement the patients own production of P. Additionally, N may be used to produce the colon cancer-associated Ps. by inserting the nucleic acids into a host cell and culturing the cell to express the proteins. N and P can be used in the prevention, diagnosis and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204 and AAB77789 represent sequences used in the exemplification of the present invention.
                                                                                                                                                                             present invention.
N.B. Pages 666 to missing at time of
                                                                                                                                                                                                                                                                                                                                                                                                            cancer-associated nucleic acid molecules (N) and proteins (P), the proteins are collectively known as colon cancer antigens. 'cancer antigens have cytostatic activity and can be used in gen therapy and vaccine production. N and P may be used in the predictions and treatment of diseases associated with inappropriations.
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    1 CCTGAAGGGAGAGCAGGAGAGAGAGGACAGTGGCCAGAGAGGGCCTCTGGGCACTGGAGG
                                                                                                                                                       Pages 666 to 682 and page 7053 of the ing at time of publication, meaning no ID NO:1027 to 1052, 7921 and 7922.
                                            cal Similarity
1872; Conserv
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                                                                                                                                                   standard; DNA;
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                                                                 receptor; cellular signal; treatment;
        Location/Qualifiers 69..1175
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA encoding CXC chemokine receptor which, are useful for treatment of i anti-viral therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (KOCH-)
                                                                                                                                                                                                                                                                                                                                                                             Sequence
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10-SEP-1996;
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                                            GGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGTGCCCCTCTTCAACATCAACTTCTACG
                                                                                     TAGCAGACACGCTGCTGGTGCTGACACTGCCGCTCTGGGCAGTGGACGCTGCCGTCCAGT
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             CAGGAGCCCTCCTGCTGGCCTGCATCAGCTTTGACCGCTACCTGAACATAGTTCATGCCA
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DB; AAW54371.
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                                                                                                                  TTCATCTTCCCCAAGTGCGGGGAGTACAAGGCATGGCGTAGAGGGTGCTGCCCCATGAAG
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Query Match Best Local Similarity

58.5%; 100.0%;

Score 1097; DB 21; Pred. No. 4.1e-234;

Sequence

1107

BP;

163 A; 380 C;

324 <u>ن</u> 240 Τ.

0 other;

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RESULT 4
AAA30593
CC The invention relates to constitutively active, non-endogenous versions CC of endogenous human orphan G protein coupled receptors (GPCRs, AAY90643-CC AAY90677 and AAY90663-Y90687), and to DNA encoding them (AAA30709-A30743 CC and AAA30775-A30779). The mutant proteins of the invention contain a CC (IC3) and transmembrane domain 6 (TM6) A non-endogenous amino acid, X, CC is substituted for an endogenous residue in IC3 at a position 16 amino CC acids N terminal of an endogenous proline in TM6 to form a sequence CC x(AA)15-Pro. The endogenous amino acid is selected from Lys, His, Arg CC or Ala, and is preferably Lys. When the endogenous residue at this CC The 15 amino acid stretch between the substituted amino acid and the Pro CC may be endogenous. Non-endogenous, or a mixture of endogenous and CC identifying antagonists, agonists and partial agonists for use as CC pharmaceutical agents. The mutant proteins are also useful in research CC settings for elucidating the roles of the receptors in normal and codiscased conditions. Antagonists for a particular GPCR are useful for CC treating diseases and disorders associated with that receptor. Because CC the novel mutant GPCRs are constitutively active, they can be used CC directly for screening of compounds without the need for endogenous CC subjected to site-directed mutagenesis CDM, encoding a human wild-type constitution of the invention. This was cloned and CC subjected to site-directed mutagenesis CDM) to generate DNA encoding CC the corresponding mutant of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Non-endogenous constitutively activated human G protein-coupled receptors, useful for identifying agonists for use as pharmaceutical agents -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          intracellular loop 3; transmembrane domain 6; drug screening;
agonist; antagonist; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein-coupled receptor; GPCR; constitutively active;
                                 corresponding mutant of the
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DB; AAY90614.
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                             present sequence represents cDNA encoding a human wild-type an exemplification of the invention. This was cloned and site-directed mutagenesis (SDM) to generate DNA encoding nding mutant of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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                                                                                                                                        GCGCTTTGGCCCGCAACTGTGGCCGAGAAAGCAGGGTAGACGTGGCCAAGTCGGTCACCT 1223
                                                                                                                                                                                   TTGCCCTCTGCTGGACCCCCTATCACCTGGTGGTGCTGGTGGACATCCTCATGGACCTGG 1163
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                  TCCAGAGGCAGCCATCGTCTTCCCGCCGGGATTCATCCTGGTCTGAGACCTCAGAGGCCT 1403
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                                                                                                                           The invention relates to constitutively active, non-endogenous versions of endogenous human orphan G protein-coupled receptors (GPCRs, AAY90643-CC AAY90677 and AAY90683-Y90687), and to DNA encoding them (AAA30709-A30743 CC and AAA30775-A30779). The mutant proteins of the invention contain a cc mutation in a portion of the protein comprising intracellular loop 3 (IC3) and transmembrane domain 6 (TM6). A non-endogenous amino acid, X, CC is substituted for an endogenous residue in IC3 at a position 16 anino CC acids N-terminal of an endogenous proline in TM6 to form a sequence CC X-(AA)15-Pro. The endogenous amino acid is selected from Lys, His, Arg CC or Ala, and is preferably Lys. When the endogenous residue at this CC position is Lys, this residue is replaced by His, Arg or preferably Ala. CC The 15 amino acid stretch between the substituted amino acid and the Pro CC may be endogenous, non-endogenous, or a mixture of endogenous and CC mon-endogenous residues. The constitutively active GPCRs are useful for CC disentifying antagonists, agonists and partial agonists for use as CC pharmaceutical agents. The mutant proteins are also useful in research CC settings for elucidating the roles of the receptors in normal and CC treating diseases and disorders associated with that receptor. Because of the novel mutant GPCR are useful for the novel mutant GPCR are useful
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                                            the novel mutant GPCRs are constitutively active, they can be used directly for screening of compounds without the need for endogenous ligands. Sequences AAA30709- AAA30743 and AAA30775-A30779 represent encoding the mutant human GPCRs of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         G protein-coupled receptor; GPCR; constitutively active; intracellular loop 3; transmembrane domain 6; drug scree
    Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  agonist; antagonist; mutant; ss.
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  324 G;
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    T; 0 other;
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Query Match
Best Local Similarity
Matches 1096; Conser

Conservative

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58.4%; 99.9%;

Score 1095.4; Pred. No. 9.3e. 0; Mismatches

9.3e-234; ches 1;

Gaps

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DB 21; Length 1107;

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CC This sequence represents cDNA encoding human chemokine receptor CXCR3b, CC a splice variant of chemokine receptor CXCR3 (also referred to as CC CXCR3a). Chemokines are a family of small cytokines which bring about the CC creatitment of leukocytes during inflammation. The CXC chemokines CC mostly attract neutrophils, while the CC chemokines are less selective. All chemokine receptors are seven transmembrane G-protein coupled CC receptors and most are receptors for a number of chemokines, CXCR3a CC being a receptor for the CXC chemokines in the selective recruitment of CC expressed in activated, but not in resting T-lymphocytes, and may CC therefore play an important role in the selective recruitment of CC CXCR3b may have an altered pattern of tissue distribution and CC CXCR3b may have an altered pattern of tissue distribution and CC CXCR3b are useful for identifying ligands, especially agonists and CC CXCR3b are useful for identifying ligands, especially agonists and CC cxCR3b are identification of chemokines responsible for mediating CC inflammatory responses is of therapeutic benefit in many conditions CC such as rheumatoid arthritis, psoriasis, multiple sclerosis, atherosclerosis. CC and restenosis.
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This represents a rodent chemokine receptor HST01.1 nucleotide sequence. The invention provides novel primate and rodent chemokines and chemokines receptors. The chemokines, receptors and binding compounds (optionally cantibodies/fragments specifically binding the chemokines) are useful therapeutically to treat conditions associated with abnormal physiology or development e.g. inflammatory conditions such as asthma. Chemokines care important in immune and inflammatory responses in that they induce leukocyte migration and adhesion. They are also chemoattractants for several cells involved in inflammation and can induce other biological responses e.g. modulation of second messenger levels (e.g. Ca++), cellular morphology modification responses, phosphoinositide lipid turnover, possible antiviral responses etc. The chemokine receptors of the invention exhibit structural properties of c-protein coupled receptors (GPCR), although their ligands have not yet been identified. The chemokine and chemokine receptor polypeptides are useful to produce ligand: receptor complexes in vivo or in assay techniques. Assays may
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rodent and primate chemokines and chemokine receptors - useful diagnostically and therapeutically to treat conditions associated with abnormal physiology or development e.g. inflammatory conditions
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 3; Pages 89-92;
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/product= "chemokine receptor HST01.1"
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Pred. No. 5.7e-178;
0; Mismatches 326;
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  Holmes
                                           29-MAR-1991;
19-DEC-1991;
                                                                                                                                                                                                               IL-8R; G-protein coupled receptor family; rhodopsin superfamily;
pro-inflammatory cytokine; 8rr.9; ss.
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                      (GETH ) GENENTECH
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  Lee
                                                                                                                                                                                                                                              factor 4 receptor superfamily member PF4AR11.
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                                           91US-0677211
91US-0810782
                                                                                                                                      Location/Qualifiers
369..1487
/*tag= a
/product= PF4ARii
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Best Local Sim
Matches 507;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The II-8 receptor cDNA sequence was isolated (see AAQ29505) and a 874bp sub-fragment of the coding sequence was used as a probe to screen human cell line HL60 and human peripheral blood lymphocyte cDNA libraries. Two new gene sequences were found that are clearly related to the II-8 receptor. One of these was contained in clone 8rr.9 and is predicted to encode an amino acid sequence which is 36% and 38% identical with the high and low affinity II-8 receptor sequences, respectively. See also AAQ37107.
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P-PSDB; AAR27793.
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                                                                                 GCTGCCCCTGCTGGTCATGGCCTACTGCTATGCCCACATCCTGGCCGTGCTG----CTGGT 1044
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                               TGCCCTCTGCTGGACCCCCTATCACCTGGTGGTGCTGGTGGACATCCTCATGGACCTGGG
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                                                                                                                              GCTGCCCATGCTGGTGATGGGCTGGTGCTACGTGGGGGTAGTGCACAGGTTGCGCCAGGC
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57.0%;
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Pred. No. 9.8e-44;
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         chronic lung inflammation. When immobilised, these anticontrolled lung inflammation. When immobilised, these acceptor in cells and be used to detect interleukin-8 receptor B expression in cells and tissues and for affinity purification of interleukin-8 receptor B from cells. This sequence is an additional chemokine superfamily receptor which was identified by probing lamda libraries of genomic DNA from a human monocyte-like cell line (L-60) and human peripheral blood lymphocytes using a large fragment of the interleukin-8 type A receptor DNA (See AAQ99006).
                                                                                                                    to treat or prevent inflammation e.g. psoriasis, dermatitis, rheumatoid arthritis and particularly inflammatory bowel disease chronic lung inflammation. When immobilised, these antibodies may be a supported by the chronic lung inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rheumatoid arthritis; inflammatory bowel diseas
chronic lung inflammation; treatment; antibody;
affinity purification; detection; ss.
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 Sequence 1679
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P-PSDB; AAR92239.
                                                                                                                                                                                                                                                                                                                 Chuntharapai A,
                                                                                                                                                                                                                                                                                                                                                                      (CHUN/)
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                                                                                                                                                               Antibodies directed against the interleukin-8 receptor B can be
                                                                                                                                                                                          Example 2; Columns
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                                                                                                                                                                                                                                                New antibodies
                                                                                                                                                                                                                                                                                                                                                                                                               25-FEB-1994;
29-MAR-1991;
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                                                                                                                                                                                                                                                                                                                                              (LEEJ/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-MAR-1991;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
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                                                                                                                                                                                                                                prevent inflammation, also
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HEBERT C.
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91US-0677211
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                                                                                                                                                                                                                                                                                                                   Hebert
327 A; 532 C; 457
                                                                                                                                                                                        51-54; 62pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         inflammation;
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detecting
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363 T; 0
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other;
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Best Local Similarity Matches 507; Conserv

Conservative

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Mismatches

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12.8%; 57.0%;

Score 240; Pred. No. 9. Score

.8e-44; DB 16;

Length Indels

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Query Match

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                           Human lymphocyte PF4AR cDNA
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Interleukin-8 receptor; IL-8 receptor;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Treatment of inflammatory disorders - by administering an antibody capable of binding a platelet factor 4 superfamily receptor polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               platelet factor superfamily receptor; lymphocyte; chemotactic; inflammation; inflammatory disease; arthritis; emphysema; cystic; fibrosis; colitis; bronchitis; meningitis; therapeutic; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1679 BP; 327 A; 532 C; 457 G; 363 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 56-58; 83pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chuntharapai A,
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                                                                                                                                                                                                                                                                                                             CAACGGCGCGGTGGCAGCCGTGCTGAGCCGGCGGGGACAGCCCTGAGCAGCAGCACAC
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                                                  CACCTGCCTGGCTGTCTGGGGGGCTCTGCCTTTTCGCCCTCCCAGACTTCATCTTCCT
                                                                                          CCTGAACATAGTTCATGCCACCCAGCTCTACCGGCGGGGGCCCCCGGCCGCGTGACCCT
                                                                                                                                CTTCAACATCAACTTCTACGCAGGAGCCCTCCTGCTGCTGCATCAGCTTTGACCGCTA
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GTCGGCCCACCACGACGAGCGCCTCAACGC----
                         CACCTGTGGGACCATCTGGCTGGTGGGCTTCCTTCCTTGCCTTGCCAGAGATTCTCTTCGC
                                                                              GGCCGAGGGCTCTGGGGTCCTGGGGACCTTCCTCTGCAAAACTGTGATTGCCCT
                                                                                                                                                                                                                                                                   CTTCCTGCTCCACCTAGCTGTAGCAGACACGCTGCTGGTGCTGACACTGCCGCTCTGGGC
                                                                                                                                                                                                                                                                                             CAACGTCCTGGTGGTGATCCTGGAGCGGCACCGGCAGACACGCAGTTCCACGGAGAC
                                                                                                                                                                                                                                                                                                                                                  CTTCAAGGCCGTGTTCGTGCCCGTGGCCTACAGCCTCATCTTCCTCCTGGGCGTGATCGG
                                                                                                                                                                                                               AGTGGACGCTGCCGTCCAGTGGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGTGCCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers 369..1487
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Pred. No. 9.8e-44;
                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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-CACCCACTGCCAATACAA
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RESULT 11
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The invention relates to constitutively active, non-endogenous versions of endogenous human orphan G protein-coupled receptors (GPCRs, AAY90643-AAY90677 and AAY90683-Y90687), and to DNA encoding them (AAA30709-A30743 and AAA30775-A30779). The mutant proteins of the invention contain a
                                                                                                             receptors,
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                                                                             Example 1;
                                                                                                                   Non-endogenous constitutively activated human G protein-coupled receptors, useful for identifying agonists for use as pharmaceus
                                                                                                                                                                                                                                                              13-OCT-1998;
                                                                                                                                                                                                                                                                                         12-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human G protein-coupled receptor BLR1 cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAA30626 standard;
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                                                                                                                                                                                                                                 (AREN-) ARENA PHARM INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                protein-coupled receptor; GPCR; constitutively active;
                                                                                                                                                             2000-329165/28
DB; AAY90627.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTTCCGCAGTGACCTGTCGCGGCTCCTGACGAAGCTGGGCTGTACCGGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGGCCTGGGCTACATGCACTGCTGCCTCAACCCGCTGCTCTATGCCCTTTGTAGGGGTCAA 1284
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTTCCTCTGCTGGTCACCCTACCACATCGTCATCTTCCTGGACACCCTGGCGAGGCTGAA 1231
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                                                                                                                                                                                                       DP,
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                                                                        Page 151; 341pp; English
                                                                                                                                                                                                       Chalmers
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                                                                                                                                                                                                                                                                                                                                                                                                                  loop 3; transmembrane domain 6; drug screening;
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CC (IC3) and transmembrane domain 6 (TM6). A non-endogenous amino acid, X, CC is substituted for an endogenous residue in IC3 at a position 16 amino CC acids N-terminal of an endogenous proline in TM6 to form a sequence CC X-(AA)15-Pro. The endogenous amino acid is selected from Lys, His, Arg CC or Ala, and is preferably Lys. When the endogenous residue at this CC position is Lys, this residue is replaced by His, Arg or preferably Ala. CC The 15 amino acid stretch between the substituted amino acid and the Pro CC may be endogenous, non-endogenous, or a mixture of endogenous and CC identifying antagonists, agonists and partial agonists for use as CC pharmaceutical agents. The mutant proteins are also useful in research CC settings for elucidating the roles of the receptors in normal and CC diseased conditions. Antagonists for a particular GPCR are useful for CC treating diseases and disorders associated with that receptor. Because CC directly for screening of compounds without the need for endogenous CC ligands. The present sequence represents cDNA encoding a human wild-type GPCR used in an exemplification of the invention. This was cloned and CC subjected to site-directed mutagenesis (SDM) to generate DNA encoding CC the corresponding mutant of the invention. This was cloned and CC subjected to site-directed mutagenesis (SDM) to generate DNA encoding CC the corresponding mutant of the invention. This was cloned and CC subjected to site-directed mutagenesis (SDM) to generate DNA encoding CC the corresponding mutant of the invention. This was cloned and CC subjected mutagenesis (SDM) to generate DNA encoding CC the corresponding mutant of the invention.
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QУ 밁 Q В δÃ Вþ δõ В Š В DЬ δõ δÃ δõ В Qy 밁 δÃ Б Qy 밁 Qy Matches 506; 1105 744 988 624 931 564 883 504 823 444 763 384 703 324 643 264 583 204 523 144 463 CTTCGACCGGGCCTTCCTGCCAGCCCTCTACAGCCTCCTCTTTCTGCTGGGGCTGCTGGG CACCTGTGGGACCATCTGGCTGGGTGGGCTTCCTCCTTGCCTTGCCAGAGATTCTCTTCGC CACCTGCCTGCCTGTCTGGGGGGCTTTTCGCCCTCCCAGACTTCATCTTCCT CCTGAACATAGTTCATGCCACCCAGCTCTACCGCCGGGGGCCCCGGGCCCGGGTGACCCT GCACAAAGTCAACTTCTACTGCAGCAGCCTGCTCCTGGCCTGCATCGCCGTGGACCGCTA CTTCCTGTTCCACCTGGCCGTGGCCGACCTCCTGCTGGTCTTCATCTTGCCCTTTGCCGT TGCCCTCTGCTGGACCCCCTATCACCTGGTGGTGGTGGACATCCTCATGGACCTGGG CCAGCGGCGCCCTCAGCGGCAGAAGGCAGTCAGGGTGGCCCATCCTGGTGACAAGCATCTT TTCCAGGGGCCAGCGGCCTGCGGGCCATGCGGCTGGTGGTGGTCGTGGTGGCCTT 1104 GCTGCCCATGCTGGTGATGGGCTGGTGGTTGGGGGGTAGTGCACAGGTTGCGCCAGGC GCTGCCCCTGCTGGTCATGGCCTACTGCTATGCCCACATCCTGGCCGTGCTG----CTGGT 1044 CCAAGCAGAAACGCATGCCTGGTTCACCTCCCGATTCCTCTACCATGTGGCGGGATTCCT CANAGTCAGCCAAGGCCATCACAACAACTCCCTGCCACGTTGCACCTTCTCCCAAGAGAA CCTGGCCATTGTCCACGCCGTCCATGCCTACCGCCACCGCCGCCTCCTCCCATCCACAT CTTCAACATCAACTTCTACGCAGGAGCCCTCCTGCTGGCCTGCATCAGCTTTGACCGCTA GGCCGAGGGCTCTGTGGGCTGGGGTCCTGGGGACCTTCCTCTGCAAAACTGTGATTGCCCT AGTGGACGCTGCCGTCCAGTGGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGTGCCCT CTTCCTGCTCCACCTAGCTGTAGCAGACACGCTGCTGGTGCTGACACTGCCGCTCTGGGC CAACGTCCTGGTGCTGGTGATCCTGGAGCCGGCACCGGCAGACACGCAGTTCCACGGAGAC CAACGGCGCGGTGGCAGCCGTGCTGAGCCGGCGGACAGCCCTGAGCAGCACCGACAC CTTCAAGGCCGTGTTCGTGCCCGTGGCCTACAGCCTCATCTTCCTCCTGGGCGTGATCGG Conservative 0; Mismatches 366; Indels 18; Gaps 743 582 522 803 683 930 882 443 762 642 987 623 563 503 822 383 702 323 203

represent DNAs

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CC AAY90677 and AAY90687), and to DNA encoding them (AAA30709-A30743 CC and AAA90769-A90789). The mutant protein of the invention contain a mutation in a portion of the protein comprising intracellular loop 3 CC (IC3) and transmembrane domain 6 (TM6). A non-endogenous amino acid, x, CC is substituted for an endogenous residue in IC3 at a position 16 amino CC acids N-terminal of an endogenous proline in TM6 to form a sequence CC x-(AA)15-Pro. The endogenous amino acid is selected from Lys, His, Arg CC or Ala, and is preferably Lys. When the endogenous residue at this CC position is Lys, this residue is replaced by His, Arg or The 15 amino acid stretch between the substituted amino acid and the Pro CC may be endogenous, non-endogenous, or amixture of endogenous and CC non-endogenous residues. The constitutively active GPCRs are useful for identifying antagonists, agonists and partial agonists for use as CC pharmaceutical agents. The mutant proteins are also useful in research CC settings for elucidating the roles of the receptors in normal and CC diseased conditions. Antagonists for a particular GPCR are useful for treating diseases and disorders associated with that receptor. Because
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               밁
                                                                                                                                                                                                                                                                                                       The invention relates to constitutively active, non-endogenous versions of endogenous human orphan G protein-coupled receptors (GPCRs, AAY90643-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     agonist; antagonist; mutant;
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                                                                                                                                                                                                                                                                                                                                                                                                                  Non-endogenous constitutively activated human G protein-coupled receptors, useful for identifying agonists for use as pharmaceutical
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA encoding human mutant G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTTCCGCAGTGACCTGTCGCGGCTCCTGACCAAGCTGGGCTGTACCGGCC 1033
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GTTCCGCAGTGACCTGTCGCGGCTCCTGACCAAGCTGGGCTGTACCGGCC
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                                                              GTTCCTGGGCCTGGCCCACTGCTCAACCCCATGCTCTACACTTTCGCCGGCGTGAA
                                                                                             AGGCCTGGGCTACATGCACTGCTGCCTCAACCCGCTGCTCTATGCCTTTGTAGGGGTCAA 1284
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56.9%;
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RESULT 13

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                                                                                                                                                                  Matches
                                                                                                                                                                                                                     Sequence 2818 BP;
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                            583
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                                                                                                                                                                               Local Similarity
              CTTCCTGCTCCACCTAGCTGTAGCAGACACGCTGCTGGTGCTGACACTGCCGCTCTGGGC
                                                                                                                       CTTCGACCGGGCCTTCCTGCCAGCCCTCTACAGCCTCCTCTTTCTGCTGGGGCTGCTGGG 522
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                                                                               CAACGGCGCGGTGGCAGCCGTGCTGAGCCGGCGGCGACAGCCCTGAGCAGCACCGACAC
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CTTCCTGTTCCACCTGGCCGTGGCCGACCTCCTGCTGGTCTTCATCTTGCCCTTTGCCGT
                                                    CAACGTCCTGGTGCTGGTGATCCTGGAGCGGCACCGGCAGACACGCAGTTCCACGGAGAC
                                                                                                         CTTCAAGGCCGTGTTCGTGCCCGTGGCCTACAGCCTCATCTTCCTCCTGGGCGTGATCGG
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                                                                                                                                                                                                                     615 A; 874
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                                                                                                                                                                             12.7%;
56.9%;
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                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Burkitt's Lymphoma
                                                                                                                                                                            Score 238.4;
Pred. No. 2.6
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                                                                                                                                                                Mismatches
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                                                                                                                                                                                                                  568 T; 0 other;
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                                                                                                                                                                                        DB 20;
                                                                                                                                                                366;
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                                                                                                                                                               Indels
                                                                                                                                                                                        Length 2818;
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RESULT 14
ABA09117/c
ID ABA09
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                           tissue regeneration; wound healing; infection; immune disorder; cell culture; drug screening; gene therapy; antiinflammatory; antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic;
                                                                        myeloid cell disorder; lymphoid cell disorder; asthma; arthritis; chronic inflammatory condition; proliferative retinopathy; atherosclerosis; coronary heart disease; arterial ischaemia; bone disorder; osteoporosis; vascular growth disorder;
                                                                                                                                                        Human; cytokine; cell proliferation; cell differentiation; gr
haematopoiesis regulation; tissue growth; immunomodulator; ac
inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis;
                                                                                                                                                                                                                                                                                                                          117/c
ABA09117 standard;
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               cytostatic;
                                                                                                                                            proliferation;
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                                                                                                                                                                                                                           Burkitt lymphoma receptor homologue cDNA,
             osteopathic; vasotropic; cardiant;
                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                            metastasis; cancer; tumour;
                                                                                                                                                                                                                                                                                                                            cDNA;
                                                                                                                                                                                                                                                                                                                            3620
                                                                                                                                            haematopoietic disorder;
          virucide;
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             antibacterial;
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                                                                                                                                                                                             factor;
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vulnerary; antiulcer;

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                                                                                                                                                                                            Sequences ABB10981-ABB12330 represent nucleic acids encoding them. The CR sequences ABA0825-ABA09574 represent nucleic acids encoding them. The CR invention also relates to vectors and recombinant host cells comprising a connected of the invention, methods of producing the novel polypeptides, can tibodies against the polypeptides, methods of identifying compounds which the polypeptides of the invention. Although novel, many of the polypeptides in a sample, and methods of identifying compounds which the polypeptides of the invention. Although novel, many of the polypeptides in a sample, and methods of identifying compounds which the polypeptides of the invention may the novel proteins, thereby considered activities, and hence the polypeptides of the invention may the polypeptides of the invention activities, including cytokine, cell proliferation or cell of the protein of the polypeptides of the invention of their biological activities; or may be conditions or chemokactic or chemokactic or chemokactic activities; receptor or ligand activities; or may be conditions, e.g., by protein or gene therapy. Such conditions include and invention are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Such conditions include cancers, haematopoletic disorders (e.g., myeloid or lymphoid cell cancers, haematopoletic disorders (e.g., myeloid or lymphoid cell cancers, haematopoletic activities may be used to promote wound healing (e.g., of burns, inclusions and ulcers), while those with the conditions in addition to immune disorders (e.g., myeloid or corrosity, and abnormal conditions with growth factor activity may be used in cell cultures to manipulate stem cells in culture to give rise to neuroepithelial cells cancers in the diagnosis of the above conditions, and in drug conditions. The present sequence represents a cDNA encod
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                                                                           Matches
3393 CTTCAAGGCCGTGTTCGTGCCCGTGGCCTACAGCCTCATCTTCCTCCTGGGCGTGATCGG
                                                                                                                                                    Sequence
                                                                                                                                                                                          novel human polypeptide of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 779-780; 1963pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          03-FEB-2000; 2000US-0496914
27-APR-2000; 2000US-0560875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human proteins and DNA encoding sequences useful for preventing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-FEB-2001; 2001WO-US03800
                             463 CTTCGACCGGGCCTTCCTGCCAGCCCTCTACAGCCTCCTCTTTCTGCTGGGGCTGCTGGG 522
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                                                                                             Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ameliorating a medical condition in a mammalian subject tis and cancer -
                                                                                                                                                      ВP;
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56.9%;
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                               Oryctolagus cuniculus
                                                                                                  Sequence encoding a high affinity recombinant rabbit interleukin-8 (IL-8) receptor polypeptide in F3R.
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                                                                                                                                                          04-APR-1993
                                                                                                                                                                                                                                 AAQ30011 standard;
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                                                                                                                                                                                                                                                                                                                                                       GTTCCGGGAGCGGATGTGGATGCTGCTCTTGCGCCTGGGCTGCCCCCAACC 1334
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCTGAACATAGTTCATGCCACCCAGCTCTACCGCCGGGGGGCCCCGGGCCCGGGGGGCCCT 822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCACAAAGTCAACTTCTACTGCAGCAGCCTGCTCCTGGCCTGCATCGCCGTGGACCGCTA
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                                                                                                                                                         (first entry)
                                                                   polypeptide;
                                                                                                                                                                                                                                 cDNA;
                                                               G-protein-coupled
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Key

Location/Qualifiers

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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (REPK )
(UYBO-)
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09-JUL-1991;
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               C---ACTTGGTCAAGTTCATATGTCTGGGCATCTGGGCGCTGTCTCTGATTTTGTCCCTG
                                                                       ATCAGCTTTGACCGCTACCTGAACATAGTTCATGCCACCCAGCTCTACCGCCGGGGGCCCC
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DB; AAR28272.
                                                        ATCAGTGTGGACCGCTACCTGGCCATTGTCCATGCTACTCGCACACTGACCCAGAAGCGC
                                                                                                                  AAGGTGGTCTCGCTTGTGAAGGAAGTCAACTTCTACAGTGGAATCCTGCTCCTGGCCTGC
                                                                                                                                             AAAGTGGCAGGTGCCCTCTTCAACATCAACTTCTACGCAGGAGCCCTCCTGCTGGCCTGC
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91US-0726606.
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CAAAACTTTCGCAATGGATTCCTCAAGATGCTTGCGGCCCGCGGC
                                            GTCAAGTTCCGGGAGCGGATGTGGATGCTGCTCTTGCGCCTGGGC 1324
                                                                                                               ACCTCAGGCCTGGGCTACATGCACTGCTGCCTCCAACCCGCTGCTCTATGCCTTTTGTAGGG
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                                                                                        ACCGAGATTCTGGGCTTCCTGCACAGCTGCCTCAACCCCATCATCTACGCCTTCATTGGC 1049
                                                                                                                                                                             ACCCACGTGATCCAGGAGACGTGTCAGCGTCGCAATGACATTGACCGGGCCCTGGACGCC
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Result
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Listing first 45 summaries
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ALIGNMENTS

ACCESSION VERSION KEYWORDS RESULT 1 BI911171 LOCUS SOURCE ORGANISM FEATURES COMMENT REFERENCE DEFINITION TITLE AUTHORS JOURNAL source Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; 1 to 864)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (1999)

Contact: Robert Strausberg, Ph.D. Plate: LLAM11532 row: g column: High quality sequence start: 3 High quality sequence stop: 788. Location/Qualifiers found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov http://image.llnl.gov g column: 11 EST BI911171.1 GI:16174778 mRNA sequence. 603062744F1 NIH_MGC_118 BI911171 Homo sapiens numan /note-"Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source leukocytes from anonymous pool of non-activated adult donors. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:5212066" /clone_lib="NIH_MGC_118" /tissue_type="leukocyte" /lab_host="DH10B" /note="Vector: pCMV-SPOR Homo 864 bp mRNA linear EST 16-OCT-20 sapiens cDNA clone IMAGE:5212066 5', mRNA Gene Collection (MGC) Hominidae; linear Euteleostomi; EST 16-OCT-2001 be

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mRNA sequence.
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Tissue Procurement: Life Technologies, Inc.
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National Institutes of Health, Mammalian
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/clone="IMAGE:5203512"
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Clone distribution: MGC clone distribution information
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11438 row: n column: 09
High quality sequence stop: 747.
LOCATION/Qualifiers
                                                                                                                                                                                                                                                                                                                     Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium
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603035039F1 NIH_MGC_115
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National Institutes of Health, Mammalian
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                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5176136"
/clone_lib="NIH_MGC_115"
/lab_host="DH10B"
/note-*Organ: pooled brain, lung, testis; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: ECORV (destroyed); RNA source anonymous pool of 6 male brains, age age 23-27; 1 male lung, age 27; and 1 male testis, age 69. Library is oligo-dT primed and directionally cloned (ECORV site is destroyed upon cloning). Average insert size 18 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C.
                                                                                                                                                                                                                                                                                                                                                                                        Strausberg, Ph.D.
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similar to SW:CCR3_HUMAN P
mRNA sequence.
AI587350
AI587350 GI:4573791
EST.
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Eukaryota; Metazoa; (
Mammalia; Eutheria; I
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NCI-CGAP http://www.r
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I Homo sapiens of P49682 C-X-C of RN.
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                 TATTTGGTCTTTTATTTTTATGTCTAAAATCCTGCTTAAAACTTTTCAATAAACAAGATC 1859
                                                                               AAGCCACAGCCCAGGCCTCCAGCTCAGCAGTGACTGTGGCCATGGTCCCCAAGACCTCTA 1799
                                                                                                                                           CATCCTGCCGCCGAGGTGGCTGCCTGGAG-CCCCACTGCCCTTCTCATTTGGAAACTAA 1679
                                                                                                                                                                                                                                                      GGAAGCCACCCTCCCAGCTTGAGGANTGCACCATTGNTGCTCCTTAGCTGCCAAGCCC
                                                                                                                                                                                                                                                                                                                    CTCTCCCCAATATCCTCGCTCCCGGGACTCACTGGCAGCCCCAGCACC-CCAGGTCTCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TATGCCTTTGTAGGGGCAAGTTTCCGGGAACGGAATGTGGATGCTGCTCTTTGCGCCTGG 558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    570;
                                                                                                                                                                                                                                                                          GGGAAGCCACCCTCCCAGCTCTGAGGACTGCACCATTGCTGCTCCTTAGCTGCCAAGCCC 1620
                                                                                                                                                                                                                                                                                                                                                 CTCTCCCCAATATCCTCGCTCCCGGGACTCACTGGCAGCCCCAGCACCACCAGGTCTCCC 1560
                                                                                                                                                                                                                                                                                                                                                                                                                                            TGGGTTTGAACCTCAGAAGGCCTCCTACTCGGGCTTGTGAGGCCGGAATCCGGGCTCCCC
                                                                                                                             AACTTCATCTTCCCCAAGTGCGGGGAGTACAAGGCATGGCGTAGAGGGTGCTGCCCCATG
                                                                                                                                                                                                                                                                                                                                                                                TTTCGCCCACAGTTTNACCTCCCGGCATTNCAGGCTCCTCCTCCCCTTTGCCGGNTNTGG
                                                                                                                                                                                                                                                                                                                                                                                                GGCTGCCCCACCAGAAAAGGGGGCTCCAGAGGCAGCCATCTCTTTCCGCCCGGGATTCATC 498
    TATTTGCTCTTTTATTTTTATGTCTAAAATCCTGCTTAAAACTTTTCAATAAACAAGATC
                                                               AAGCCACAGCCCAGGCCTCCAGCTCAGCAGTGACTGTGGCCATGGTCCCCCAAGACCTCTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Life Technologies catalog #: 11548-013
DNA Sequencing by: Washington University Genome
Clone distribution: NCI-CGAP clone distribution
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1908 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seq primer: -40UP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      National Cancer Institute, Cancer Genome
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Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.72 kb. Life Technologies catalog #:
11548-013"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2224726"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="adenocarcinoma"
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Pred. No. 8.
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Best Local Similarity
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                                                                                                                                                       GTTGCCGCCCTCCTGGAGAACTTCAGCTCTTCCTATGGACTATGGAGAAAACGAGAGTGAC 418
                                                                                                                                                                                                               CGTACCAGCCCAGCTATGGTCCCTGAGATGAGTGAACGCCAAGAGTTCCAAGCCTCCGAT 76
                   CTGCCAGCCCTCTACAGCCTCCTCTTTCTGCTGGGGCTGCTGGGCCAACGGCGCGGTGGCA 538
                                                                           TCGTGCTGTACCTCCCCGCCCTGCCCACAGGACTTCAGCCTGAACTTCGACCGGGCCTTC 478
                                                       TTCTGCTGTACTTCCCCACCCTGCCCACAGGACTTCAGCCTCAACTTCGACCGCACCTTC
                                                                                                                                   TTTGCCTACCTCCTGGAAAA-----CTCTTCCTATGACTACGGAGAAAATGAGACCTAC 130
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Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T., Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett,G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A., Chitko-McKown,C.G. Pertea,G., Holt,I., Karamycheva,S., Liang,F., Quackenbush,J. and Keele,J.W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, US
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BI975807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plate: 110 row: A column: 16 Seq primer: ATTTAGGTGACACTATAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTTCCCAGTCACGACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: 402 762 4366
Fax: 402 762 4390
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
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199 c 152 g 135 t
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Library made from pooled tissue from testis, thymus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="MARC 2BOV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="pooled"
/lab_host="DH10B"
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McKown, C.G.,
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E 21180013

E CONTACT: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed wit v0.980904.e. Vector identified by cross_match with the and -minmatch 12 options.
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                                                                                                                                                              and minmatch 12 options.
PCR PRIMERS
FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTTCCCAGTCACGACG
Plate: 86 row: D column: 24
Seq primer: ATTTAGGTGACACTATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and
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106015 MARC 1BOV
AW655246
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Sequence evaluation of four
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                                                                                                                                               te: 86 row: D column: 24 primer: ATTTAGGTGACACTATAG Location/Qualifiers
                                                 /organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="MARC 1BOV"
/tissue_type="pooled"
/lab_host="DH10B"
/note-"Vector: pCMV SPORT6; Site_1: xbaI; Site_2: XhoI; Library made from pooled tissue from lymph node, ovary, fat, hypothalamus, and pituitary."
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417; Conserv
                                                                                                                                            Via U. Bassi 58/B, 35121 Padua, Italy sequencing centre identifier: HSPD50322 ABI Chromatograms and other information http://muscle.cribi.unipd.it
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AJ346279
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                                                                                                                                                                                                                           Unpublished (2001)
Contact: Laveder P
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Laveder, P., De Pitta, C.,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 348)
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/tissue_type="pectoral muscle (after mastectomy)"
/note="Vector: pOPD (Custom); Site_1: EcoR1; Site_2: Not
caucasian; Skeletal muscle cDNA was depleted of hundred
most expressed mRNAs through an original two steps
                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="HM3/S3"
/sex="female"
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                                                                                                                                                                                                                                                                                                                                                                                 maa56a05.yl Soares mouse 3NbMS Mus musculus cDNA clone
IMAGE:3826689 5' similar to TR:088410 088410 CHEMOKINE RECEPTOR
CXCR3. [1] ;, mRNA sequence.
BF452722
BF452722.1 GI:11518891
EST.
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340; Conserv
                                                                                                                                                                                                                    Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Contact: Cappbs-r@mail.nih.gov
Email: cgapbs-r@mailable royalty-free through LLNL;
This clone is available royalty-free through LLNL;
                                                                                                                                                                                                                                                                                             Mammalia; Eutheria; Rodentia; Sciurognathi; Murid
1 (bases 1 to 468)
NCI-GGAP http://www.ncbi.nlm.nih.gov/nciogap.
National Cancer Institute, Cancer Genome Anatomy
                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
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Seq primer:
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                                                                                                                                                                                                                                                                                                                                                            Mus musculus
                                                                                                                                                                        High quality sequence stop:
Location/Qualifiers
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                                                                                                                                                                                                 primer: -40RP from Gibco
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a 110 c
/lab_host="DH10B"
/note="Vector: pT73D-Pac (Pharmacia) with a modified /note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDN was primed with a Not I - oligo(dT) primer [5' was primed with a Not I - oligo(dT) primer [5']
                                                                                                             /db_xref="taxon:10090"
/clone="IMAGE:3820689"
                                                                                                                                     /organism="Mus musculus"
/strain="C57BL/6J"
                                                            /tissue_type="Spleen"
/dev_stage="4 weeks"
                                                                                     /clone_lib="Soares mouse
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18.1%;
99.7%;
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Pred. No. 1.2e
0; Mismatches
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324 AGGTGAGTGACCACCAAGTGCTAAATGACGCCGAGGTTGCCGCCCTCCTGGAGAACTTCA 383
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                                                                                                                                  Contact: Sonstegard TS USDA, ARS, Beltsville Agricultural Research Bdlg. 200 Rm 2A, Beltsville, MD 20705, USA Tel: 301 504 8416
Fax: 301 504 8414
                                                                                                                                                                                                                                   gland cDNA library
Unpublished (2000)
                                     and -minmatch 12 options. PCR PRimers
                                                                            Email: tads@lpsi.barc.usda.gov
Single pass sequencing. Bases v0.980904.e. Vector identified
                                                                                                                                                                                                                                                                            Wells, K.D.
Mapping of Expressed
                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 511)
Sonstegard, T.S., Ca
                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora;
                                                                                                                                                                                                                                                                                                                                                             Bovidae; Bovinae; Bos.
                FORWARD: AGGAAACAGCTATGACCAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not and Eco RI sites of the modified pT7T3 vector. RNA provided by Dr. Bertrand Jordan. Library went through three rounds of normalization, and was constructed by Bento Soares and M.Fatima Bonaldo."
GTTTTCCCAGTCACGACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5BOV Bos taurus cDNA
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Pred. No. 8.8e-47;
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                         Unpublished (1997)
other ESTs: maa56a05.yl
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                           PR453946 TOB bp mRNA linear EST 01-DEC-7 maa56a05.x1 Soares mouse 3NbMS Mus musculus cDNA clone IMAGE:3820689 3' similar to TR:088410 088410 CHEMOKINE RECEPTOR CXCR3. [1] ;, mRNA sequence.
EF453946 BF453946.1 GI:11520115
                                                                                                                                                            Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; leukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; 1 (bases 1 to 708)
MGI:1457041
High qualit
                                                                                                                                 Tumor Gene Index
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National Cancer Institute, Cancer Genome Ana
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quality sequence stop: 444
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Library made from pooled mRNA isolated from mammary
tissues at eight physiological, developmental, and disease
states."
a 167 c 135 g 112 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="BARC 5BOV"
/tissue_type="pooled"
/lab_host="DH10B"
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Pred. No. 4.1
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                                                                                                                                                                                                                                                                TCCTGGTCTGAGACCTCAGAGGCCTCCTACTCGGGCTTGTGAGGCCGGAATCCGGGCTCC 1438
                                                                                                                                                                                                                                                                                                                                                                 CTGGGCTGCCCCAACCAGAGAGGCCTCCAGAGGCAGCCATCGTCTTCCCGCCGGGATTCA 1378
                                                                                                                                                                                                                                                                                                                                                                                                                  CTGCTCTATGCCTTTGTAGGGGTCAAGTTCCGGGAGCGGATGTGGATGCTGCTCTTGCGC 1318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTAGACGTGGCCAAGTCGGTCACCTCAGGCCTGGGCTACATGCACTGCTGCTCAACCCG 1258
GCGTTGTCAGCACTG
                       CCCATGAAGCCACAG 1748
                                                                        AACTAAAACTTCATCTTCCCCAAGTGCGGGGGGTACAAGGCATGGCGTAGAGGGTGCTGC
                                                                                                  AGCCCCATCCTGCCGCCCGAGG--TGGCTGCCTGGAGCCCCACTGCCCTTCTCATTTGGA 1673
                                                                                                                                                                                                                          CTGGCTCTCCCCAATATCCTCGCTCCCGGGACTCACTGGCAGC-CCCAGCACCACCAGGT 1555
                                                                                                                                                                                                                                                  GCCTGCGCAGCCCAAGTCCTAACACACTCCAAGTGCTTGTCCTCCTTGTAGTTGGGCTAG
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/db_xref="taxon:10090"
/clone="IMAGE:3820689"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="Spleen"
/dev_stage="4 weeks"
/lab_host="DH108"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="Soares mouse
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Pred. No. 1.1e-44;
0; Mismatches 185;
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                 GCCGTGCTGAGCCGGCGGACAGCCCTGAGCAGCACCGACACCTTCCTGCTCCACCTA 598
                                                                                         CTGCCAGCCCTCTACAGCCTCCTTTCTGCTGGGGCTGCTGGGCAACGGCGCGGTGGCA 538
                                                                                                                                                                  TCGTGCTGTACCTCCCGCGCCTGCCCACAGGACTTCAGCCTGAACTTCGACCGGGCCTTC 478
                                                                                                                                                                                                                   TTTGCCTACCTCCTGGAAAA-----CTCTTCCTATGACTACGGAGAAAATGAGACCTAC
                                                                                                                                                                                                                                      GTTGCCGCCCTCCTGGAGAACTTCAGCTCTTCCTATGACTATGGAGAAAACGAGAGTGAC 418
                                                                                                                                                                                                                                                                                                               CCTTCCTCCCCGTTCCCGCCCTCACAGGTGAGTGACCACCAAGTGCTAAATGACGCCGAG 358
GTCGTGCTGAGCCAGAGGGCGGCCCTGAGCAGCACCGACACCTTTCTGCTGCACTTG
                                                                      CTGCCCGTCCTCTACAGCCTCCTCTTTGTGCTGGGGCTTCTGGGTAATGGCATCGTGGCA
                                                                                                                                               TTCTGCTGTACTTCCCCCACCCTGCCCACAGGACTTCAGCCTCAACTTCGACCGCACCTTC
                                                                                                                                                                                                                                                                                            CGTACCAGCCCAGCTATGGTCCCTGAGATGAGTGAACGCCAAGAGTTCCAAGCCTCCGAT 85
                                                                                                                                                                                                                                                                                                                                                                      297;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 6893-0166, USA Tel: 402 762 4360 Fax: 402 762 4390 Email: smith@email.marc.usda.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BACKWARD: GTTTTCCCAGTCACGACG
Plate: 23 row: J column: 5
Seq primer: ATTTAGGTGACACTATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Single pass sequencing. Bases called and trimmed with phred v0.980904.e. Vector identified by cross_match with the -min. and -minmatch 12 options.
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Contact: Smith TPL
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Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36085 MARC 1BOV Bos taurus
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EST.
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              70
                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: Library made from pooled tissue from lymph node, c fat, hypothalamus, and pituitary."
131 c 102 g 89 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="MARC 1BOV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="pooled"
/lab_host="DH10B"
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79.6%;
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Pred. No. 1.1e-39;
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AUTHORS
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GACCGCTACGTAGCCATCCACGCCGTGTCGGCTCATCGCCACCGCGCCCGCGTGCTT
                                     GACCGCTACCTGAACATAGTTCATGCC-----ACCCAGCTCTACCGCCGGGGGCCCCCG
                                                                        TTTGGCATCTATAAGTTAAGCTTCTTCAGCGGGATGCTGCTGCTCCTATGCATCAGCATT
                                                                                                                                            TTCTGGGCCTACAGCGAAGCCAAGTCCTGGATCTTTGGCGTCTACCTGTGTAAGGGCATC
                                                                                                                                                                               CTCTGGGCAGTGGACGCTGCCGTCCAGTGGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCA 694
                                                                                                                                                                                                                     ACGGATACCTACCTGCTCAACCTGGCCGTGGCAGACATCCTTTTCCTCCTGATTCTTCCC 60
                                                                                                                                                                                                                                                                                          417;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BI653693
603300354F1 NIH_CGAP_Mam3 Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     found through the I.M.A.G.E. Consortium/LLNL http://image.llnl.gov
Plate: LLAM11865 row: 1 column: 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                  164
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Location/Qualifiers
                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                          /note-"organ: mammary; Vector: pCMV-SPORT6; Site_1: NotI; Slte_2: SalI; Cloned unidirectionally, Primer: Oligo dT. Recarge insert 2 kb. Library constructed by Life Technologies, catalog #12017-018. Investigators providing samples: Lothar Hennighausen/Chu-xia Deng, NIH Reference for transgenic model: Xu et al., Nature Genetics 22, 37-4 (1999). Note: this is a NCI_CGAP Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:5340828"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="tumor, gross tissue"
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53.2%;
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Pred. No. 9.2e-24;
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Genoscope - Centre National de So
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, 1
                                                                                                                                                                                              Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished (2001)
                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; 1 (bases 1 to 944)
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was primed with a NotI-oligo(dT) primer. Five
                          /tissue_type="neuroblastoma cells"
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                                                                                                                        463 CTTCGACCGGGCCTTCCTGCCAGCCCTCTACAGCCTCCTCTTTCTGCTGGGGCTGCTGGG 522
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                                      523 CAACGGCGCGGTGGCAGCCGTGCTGCTGAGCCGGCGGACAGCCCTGAGCAGCACCGACAC 582
                                                                                 CC 1329
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CAACATCCTGGTGCTGGTGATCCTGGAGCGGCACCGGCAAACACGCAACTCCACCGAGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FORWARD: 5'-(CUA)4GGCCACGGTCGACTAGTAC-3'
BACKWARD: 5'-(CAU)4CTGTTTGAGCGGATGAAGGTGAA-3'
Insert Length: 573 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: acacia.warren@tufts.edu
The cDNA was isolated from blood cells (buffy
Thoroughbred septic foal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: (508) 839-7970 Fax: (508) 839-7091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Department of Environmental and Population Health
Tufts University School of Veterinary Medicine
200 Westboro Road, North Grafton, MA 01536, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Alcivar-Warren, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mammalia; Eutheria; Perissodactyla; Equidae; 1 (bases 1 to 573) Pascual,I., Dhar,A.K., Fan,Y., Paradis,M.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Equus caballus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                               /note="vector: pAMP1 (Gibco BRL); Obtained by 5'RACE following the protocol of Gibco BRL. CDNA was synthesized using a gene-specific (ILL-ra) primer (GSP1: 5'-CTGTTTGAGCGGATGAAGGT-3') from a genomic sequence. dCTP was used to add a homopolymeric tail in the 3'end and the tailed cDNA was amplified by PCR using an anchor IL-1ra gene-specific primer (GSP2: 5'-CAUCAUCAUCTGTTGACCGGATGAAGGTGAA-3') as the reverse and a Universal Anchor Primer (Gibco BRL) as the forward primer. cDNA was cloned through UDG cloning method." a 135 c 200 g 100 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="TUDPEC185"
/clone_lib="5'RACE cDNA"
/tissue_type="Blood cells (buffy coat) from a septic female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /dev_stage="Foal"
/lab_host="E. coli DH5"
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                                                                                                                                                                                      8.4%;
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                                                                                                                                                              Score 158.4; DB 10;
Pred. No. 7.4e-23;
0; Mismatches 171;
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   364;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Full-length cDNA libraries and normalization Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                          Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Genoscope
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1 (bases 1 to 935)
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   Conservative
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                                                                                /note="organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies. Contact: Feng Liang Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax: (1) 301 610 8371 Email: fliang@lifetech.com URL: http://fulllength.invitrogen.com"
                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0DM003YH06"
                                                                                                                                                                                                                                                                                 /tissue_type="neuroblastoma cells"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                  /sex="male"
                                                                                                                                                                                                                                                                                                                                      /clone_lib="LTI_NFL001_NBC4"
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                8.3%;
Score 155; DB Pred. No. 3.9e 0; Mismatches
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                                                                                                                                             GCTGCAGCTGGTGGCTTTCTGCTGCCCCTGCTGGTCATGGCCTACTGCTATGCCCA 1023
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                                                                                                                                  CCTGCCTCACACCTTTGGCTTCATCGTGCCGCTGTTTGTCATGCTGTTCTGCTATGGATT 735
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                                                            CTTTGCTGTCGTCCTCATCTTCCTGCTTTGCTGGCTGCCCTACAACCTGGTCCTGCTGGC 855
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Search completed: November Job time: 1694 secs

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Minimum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Title:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB seq length: 0
DB seq length: 2000000000
Pending_Patents_NA_Main:*

1: \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) 
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Listing first 45 summaries
                         /cgn2_6/ptodata/1/pna/US082_COMB.seq:*
/cgn2_6/ptodata/1/pna/US084_COMB.seq:*
/cgn2_6/ptodata/1/pna/US084_COMB.seq:*
/cgn2_6/ptodata/1/pna/US085_COMB.seq:*
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/cgn2_6/ptodata/1/pna/US099_COMB.seq:*
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44: /cgn2_6/ptodata/1/pna/US6005_COMB.seq:  
45: /cgn2_6/ptodata/1/pna/US6006_COMB.seq:  
46: /cgn2_6/ptodata/1/pna/US6009_COMB.seq:  
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51: /cgn2_6/ptodata/1/pna/US6011_COMB.seq:  
52: /cgn2_6/ptodata/1/pna/US6011_COMB.seq:  
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67: /cgn2_6/ptodata/1/pna/US6013_COMB.seq:  
67: /cgn2_6/ptodata/1
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.

Query Score Match Length DB

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Description

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613 613		1874.4 1874.4 1874.4 1873.2 1839.2 1548.4
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Sequence 1010, Ap Sequence 25025, A Sequence 129, App Sequence 748, App Sequence 141, App	sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 211, Appli Sequence 201, Appli Sequence 1052, Appli Sequence 19, Appli Sequence 19, Appli Sequence 19, Appli Sequence 173, Appli Sequence 173, Appli Sequence 302, Appli Sequence 301, Appli Sequence 510, Appli Sequence 650, Appli	1, Ap 1, Ap 1, Ap 1, P 2115, 2115, 3, P

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PCT-US96-00499-1
PCT-US96-00499-1
; Sequence 1, Application PG GENERAL INFORMATION:
; GENERAL INFORMATION:
; TITLE OF INVENTION: HISTORY TITLE OF INVENTION: HISTORY TO THE PROPERTY OF THE PR
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Matches
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                                                                                                                    Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Carella, Byrne, Bain, Gilfillan, ADDRESSEE: Stewart & Olstein STREET: 6 Becker Farm Road CITY: Roseland STATE: NJ COUNTRY: USA ZIP: 07068-1739
COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1 CURRENT APPLICATION NUMBER: PCT/US96/00499
FILING DATE: PCT/US96/00499
FILING DATE: PCT/US96/00499
FILING DATE: PCT/US96/00499
                                                                                                                                                                                                                                                                                             TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-474
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-944-1700
                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Ferraro, Gregory D
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CORRESPONDENCE ADDRESS:
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US-60-194-091-736
US-10-029-386-35624
US-10-029-386-11311
US-09-698-013-414
US-10-029-386-17324
US-09-598-013-1151
US-09-538-409-92538
US-09-933-524-92538
US-09-933-524-92537
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US-09-933-524-92537
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US-09-933-524-92537
                                                                                                   Score 1874.4;
Pred. No. 0;
0; Mismatches
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                                                                                                                                                         Sequence 1, Application GENERAL INFORMATION:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC FLOS/MS-OOS
OPERATING SYSTEM: PC-DOS/MS-OOS
SOFTWARE: Patentin Release #1.0, V.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/00499
                                                                                                                 TITLE OF INVENTION: HE TITLE OF INVENTION: HS NUMBER OF SEQUENCES: 9 CORRESPONDENCE ADDRESS:
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CITY: Roseland
STATE: NJ
                                                                                         ADDRESSEE: Carella, Byrne, B
ADDRESSEE: Stewart & Olstein
STREET: 6 Becker Farm Road
                                                                 COUNTRY:
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MOLECULE TYPE:
FEATURE:
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ATTORNEY/AGENT INFORMATION:
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TELEFAX: 201-994-1744. INFORMATION FOR SEQ ID NO: 1:
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TELEPHONE: 201-994-1700
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LENGTH: 1876 base pair
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STRANDEDNESS: single
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APPLICANT: Li, Yi
TITLE OF INVENTION: Human G-Protein Chemoki
FILE REFERENCE: PF218PCT.US
CURRENT APPLICATION NUMBER: US/09/101,518
CURRENT FILING DATE: 1998-12-21
PRIOR APPLICATION NUMBER: PC7/US96/00499
PRIOR APPLICATION NUMBER: PC7/US96/00499
PRIOR FILING DATE: 1996-01-11
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
SECOND: 1876
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; LOCATION: (173)..(1420)
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Best Local Similarity
Matches 1875; Conserv
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ORGANISM: HOMO
FEATURE:
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APPLICATION NUMBER: 60/163,280
PRIOR FILING DATE: 1999-01-23
PRIOR FILING DATE: 1999-01-23
PRIOR FILING DATE: 1999-01-23
PRIOR FILING DATE: 1999-01-23
PRIOR APPLICATION NUMBER: 60/163,280
PRIOR APPLICATION NUMBER: 60/163,280
PRIOR APPLICATION NUMBER: 50/163,280
PRIOR PILING DATE: 1999-11-03
NUMBER OF SEQ ID NOS: 8564
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 2115
LENGTH: 1877
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Matches
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Pred. No. 0;
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US-60-258-273-3/c

Sequence 3, Application US/60258273

GENERAL INFORMATION:

APPLICANT: Beasley, Ellen

TITLE OF INVENTION: ISOLATED HUMAN NUCLEAR HORMONE

TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECUI

TITLE OF INVENTION: HORMONE RECEPTOR PROTEINS, AND

FILE REFERENCE: CLO01042-PROV

CURRENT APPLICATION NUMBER: US/60/258,273

CURRENT FILING DATE: 2000-12-27

NUMBER OF SEO ID NOS: 312

SOFTWARE: FastSEQ for Windows Version 4.0

SEO ID NO 3

LENGTH: 6604

TYPE: DNA

ORGANISM: Human

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RESULT 6
US-09-023-655-980
                                                      ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEPAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 980:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORD PERFECT 6.1 FOR WINDOWS/MS-DOS
SOFTWARE: WORD PATA:
APPLICATION NUMBER: US/09/023,655
FILING DATE: HEREWITH
CLASSIFICATION UNBER:
PRIOR APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION NUMBER:
FILING DATE:
CLASSIFICATION:
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APPLICANT: Susan G. Stuart
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FC
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
LENGTH: 1670
TYPE: nucleic
STRANDEDNESS:
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APPLICANT: HOTTE, Darci T.
APPLICANT: Vockley, Joseph G.
APPLICANT: Scherf, Uwe
APPLICANT: Scherf, Uwe
APPLICANT: Scherf, Uwe
INTITLE OF INVENTION: Gene Expression Profiles in
FILE REFERENCE: 44921-5028-W0
CURRENT APPLICATION NUMBER: US/09/880,107
CURRENT FILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR FILING DATE: 2000-06-14
PRIOR FILING DATE: 2000-10-02
INUMBER OF SEQ ID NOS: 3950
SOSTWARR: PAREONTIN VET: 2.1
SEQ ID NO 3833
LENGTH: 1670
                  ; FEATURE:
; OTHER INFORMATION:
US-09-880-107-3833
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US-09-880-107-3833
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Query Match
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ADDRESSEE: Hamilton, Brook, Smith & STREET: Two Militia Drive CITY: Lexington STATE: MA COUNTRY: USA ZIP: 02173

COUNTRY: USA ZIP: 02173

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk COMPUTER: IBM PC Compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Ve: APPLICATION NATA:

APPLICATION NUMBER: US/09/624,594
FILING DATE: 25-JUL-2000
PRIOR APPLICATION DATA: APPLICATION DATA:

APPLICATION NUMBER: US/08/709,838
FILING DATE: 10-SEP-196
ATTORNEY/AGENT INFORMATION:
NAME: Brook Esq., David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: TKI96-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
TELEPHONE: (617) 861-6240
                                                                                                                                                                                                                                                                 APPLICANT: Loetscher, Marcel
APPLICANT: Moser, Bernhard
TITLE OF INVENTION: IP-10/MIG RECEPTOR
TITLE OF INVENTION: NUCLEIC ACIDS, AND
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Best Local Similarity 99.1%;
Matches 1550; Conservative
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SEQUENCE CHARACTERISTICS:
LENGTH: 1670 base pairs
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                    GGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGTGCCCTCTTCAACATCAACTTCTACG
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Pred. No. 3.6
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Sequence 1, Application US/09633541

GENERAL INFORMATION:
APPLICANT: Loetscher, Marcel
APPLICANT: Moser, Bernhard
TITLE OF INVENTION: IP-10/MIG RECEPTOR DES
TITLE OF INVENTION: NUCLEIC ACIDS, AND MET
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reyn
STREET: Two Militia Drive
CITY: Lexington
STREET: USA
COUNTRY: USA
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFFWARE: Patentin Release #1.0, Version
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US-09-633-541-1
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APPLICATION DATA:
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           Version
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; LOCATION:
US-09-633-541-1
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NAME: Brook Esq., David E.

REGISTRATION NUMBER: 22,592

REFERENCE/DOCKET NUMBER: TK196-01

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 861-6240

TELEFAX: (617) 861-9540

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:
LENGTH: 1670 base pairs

TYPE: nucleic acid

STRANDEDNESS: double
TOPOLOGY: unknown
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 1550; Conserv
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FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
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TGCTGCAGCTGGTGGCTTTCTGCTGCCCCTGCTGGTCATGGCCTACTGCTATGCCC
                   GCCTCAACGCCACCCACTGCCAATACAACTTCCCACAGGTGGGCCGCACGGCTCTGCGGG
                                                             GGCTCTGCCTGTTTTCGCCCTCCCAGACTTCATCTTCCTGTCGGCCCACCACGACGAGC
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RESULT 10
US-09-663-702-1
; Sequence 1, Application US/09663702
; GENERAL INFORMATION:
. APPLICANT: Loetscher, Marcel
Moser, Bernhard
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TITLE

QF)

Qin, Shixin Mackay, Charles R. INVENTION: IP-10/MIG

RECEPTOR DESIGNATED CXCR3

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ACIDS,

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NAME/KEY: CDS;
LOCATION: 69..1172;
SEQUENCE DESCRIPTION: SEQUS-09-663-702-1
                                                                                                                                                                                                                                                                                                                                                                                              Matches 1550;
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TELEPHONE: (617) 861-6240
TELEPAX: (617) 861-9540
WHATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/829,
FILING DATE: - CUDKNOWN>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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 CAGGAGCCCTCCTGCTGCCTGCATCAGCTTTGACCGCTACCTGAACATAGTTCATGCCA
                                                                              TAGCAGACACGCTGCTGGTGCTGACACTGCCGCTCTGGGCAGTGGACGCTGCCGTCCAGT
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CITY: Lexington
STATE: MA
COUNTRY: USA
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TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Brook Esq., David E. REGISTRATION NUMBER: 22,592
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Pred. No. 3.6e-312;
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NAME/KEY: CDS
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LOCATION: 69..1172
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SEQUENCE DESCRIPTION: SEQ ID
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FILING DATE: 15-Sep-2000
CLASSIFICATION: Unknown>
PRIOR APPLICATION ODATA:
APPLICATION NUMBER: 08/709,838
FILING DATE: -Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: BTOOK ESQ., David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: TK196-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
TELEPHONE: (617) 861-6240
INFORMATION FOR SED ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/09663799 GENERAL INFORMATION:
                                                                                                                                                                                                Best Local Similarity Matches 1550; Conserv
                                                                                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC:DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton,
STREET: Two Militia |
                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Loetscher, Marcel
                                                                                              CCGCCCTCCTGGAGAACTTCAGCTCTTCCTATGACTATGGAGAAAACGAGAGTGACTCGT 422
          CAGCCCTCTACAGCCTCCTTTCTGCTGGGGCTGCTGGGCAACGGCGCGGTGGCAGCCG
                                                          GCTGTACCTCCCCGCCCTGCCCACAGGACTTCAGCCTGAACTTCGACCGGGCCTTCCTGC
                                                                                                                                               CCAGCCCAGCCATGGTCCTTGAGGTGAGTGACCACCAAGTGCTAAATGACGCCGAGGTTG
CAGCCCTCTACAGCCTCCTCTTTCTGCTGGGGCTGGCCAACGGCGCGGTGGCAGCCG
                                              GCTGTACCTCCCCGCCCTGCCCACAGGACTTCAGCCTGAACTTCGACCGGGCCTTCCTGC
                                                                                                                                                                       CCTCCCCGTTCCCGCCCTCACAGGTGAGTGACCACCAAGTGCTAAATGACGCCGAGGTTG 362
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                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: MA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                           TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 02173
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                                 GAAGCCACCCTCCCAGCTCTGAGGACTGCACCATTGCTGCTCCTTAGCTGCCAAGCCCCA 1622
                                                                                                                     GGTCTGAGACCTCAGAGGCCTCCTACTCGGGCTTGTGAGGCCGGAATCCGGGCTCCCCTT 1442
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Sequence 211, Application US/60258273

GENERAL INFORMATION:
APPLICANT: Beasley, Ellen
TITLE OF INVENTION: ISOLATED HUMAN NUCLEAR H
TITLE OF INVENTION: PROTEINS, NUCLEIC ACID
TITLE OF INVENTION: HORMONE RECEPTOR PROTEI
FILE REFERENCE: CLOOI042-PROV
CURRENT APPLICATION NUMBER: US/60/258,273
CURRENT TILING DATE: 2000-12-27
NUMBER OF SEQ ID NOS: 312
SOFTWARRE: FASTSEQ for Windows Version 4.0
SEQ ID NO 211
LENGTH: 1626
TYPE: DNA
ORGANISM: Human
US-60-258-273-211
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ISOLATED HUMAN NUCLEAR HORMONE RECEPTOR
PROTEINS, NUCLEIC ACID MOLECULES ENCODING
HORMONE RECEPTOR PROTEINS, AND USES THEREC
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99.0%;
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US-09-016-434-1052
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GENERAL INFORMATION:
APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
NUMBER OF SEQUENCES: 1490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORD PERFECT 6.1 for Windows/MS-DOS 6.:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION NUMBER:
FILING DATE:
APPLICATION NUMBER:
FILING DATE:
FILING DATE:
FILING DATE:
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                    Matches 1293;
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Best Local Similarity
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INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                     NAME: Zeller, Karen J.
REGISTAREN NUMBER: 37,071
REFERENCE/DOKET NUMBER: PA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
                                                                                                                                                                                                                                                                          IMMEDIATE SOURCE:
LIBRARY: GENBANK
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CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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CAAGTGCTAAATGACGCCGAGGTTGCCGCCCTCCTGGAGAACTTCAGCTCTTCCTATGAC
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US-09-960-706-962
Sequence 962, Application US/09960706
GENERAL INFORMATION:
TITLE OF INVENTION: William E.
APPLICANT: Munger, William E.
TITLE OF INVENTION: Identifying Drugs for and
TITLE OF INVENTION: Gene Expression Profilee
FILE REFERENCE: 44921-5029-01US
CURRENT APPLICATION NUMBER: US/09/960,706
CURRENT FILING DATE: 2001-09-24
PRIOR APPLICATION NUMBER: 60/223,323
PRIOR FILING DATE: 2000-08-07
PRIOR FILING DATE: 2000-08-07
PRIOR FILING DATE: 2001-06-05
NUMBER OF SEQ ID NOS: 1124
SOFTMARE: Patentin Ver. 2.1
SEQ ID NO 962
LENGTH: 1293
TYPE: DNA
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Matches 1293; Conserv
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OTHER INFORMATION:
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; Pred. No. 3.6e-260;
0; Mismatches 0;
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Sequence 19, Application US/09170496
GENERAL INFORMATION:
APPLICANT: Behan, Dominic P.
APPLICANT: Behan, Dominic P.
APPLICANT: Liaw, Chen W.
APPLICANT: Liaw, Chen W.
TITLE OF INVENTION: Non-Endogenous, ConstituTITLE OF INVENTION: Receptors
FILE REFERENCE: AREN-0040
CURRENT APPLICATION NUMBER: US/09/170,496
CURRENT FILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 286
SOFTWARE: PatentIn version 3.0
SEQ ID NO 19
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                                              58.5%;
llarity 100.0%;
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                                              Score 1097; DB 15;
; Pred. No. 3.7e-219;
0; Mismatches 0;
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1343 1030	1284 AGTTCCGGGAGCGGATGTGGATGCTGCTCTTGCGCCTGGGCTGCCCCAACCAGAGAGAG	
1283 970	1224 CAGGCCTGGGCTACATGCACTGCTGCTCCTACCCGCTGCTCTATGCCTTTGTAGGGGTCA	
1223 910	1164 GCGCTTTGGCCCGCAACTGTGGCCGAGAAAGCAGGGTAGACGTGGCCAAGTCGGTCACCT 	
1163 850	1104 TTGCCCTCTGCTGGACCCCCTATCACCTGGTGGTGGTGGTGGACATCCTCATGGACCTGG	
1103 790	1044 TTTCCAGGGGCCAGCGGCGCCTGCGGGCCATGCGGTGGTGGTGGTGGTGGTGGTGGCCT	
1043 730	984 TTCTGCTGCCCCTGCTGGTCATGGCCTACTGCTATGCCCACATCCTGGCCGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	
983 670	924 AATACAACTTCCCACAGGTGGGCCGCACGGCTCTGCGGGTGCTGCAGCTGGTGGCTGGC	
923 610	864 TCCCAGACTTCATCTTCCTGTCGGCCCACCACGACGACGACGCCTCAACGCCACCCAC	
863 550		
803 490	744 GCATCAGCTTTGACCGCTACCTGAACATAGTTCATGCCACCCAGCTCTACCGCCGGGGGC	
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563 250	504 TTCTGCTGGGCCTGCTGGGCAACGGCGGTGGCAGCCGTGCTGATGAGCCGGCGGACAG	
503 190	444 CACAGGACTTCAGCCTGAACTTCGACCGGGCCTTCCTGCCAGCCCTCTACAGCCTCCTCT	
443 130	384 GCTCTTCCTATGACTATGAGAAAAAGGAGAGTGACTCGTGCTGTACCTCCCCGCCCTGCC	

Вb

Search completed: November 2, 2002, 05:19:38 Job time: 2887 secs

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Result
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re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
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: /cgn2_6/ptodata/2/pna/PCT_NEW_COMB.seq: *
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: /cgn2_6/ptodata/2/pna/US07_NEW_COMB.seq: *
: /cgn2_6/ptodata/2/pna/US07_NEW_COMB.seq: *
: /cgn2_6/ptodata/2/pna/US08_NEW_COMB.seq: *
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: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq: *
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Listing first 45 summaries
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  US-10-172-118-620
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US-10-251-385-173
US-10-035-832-1413
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2 US-10-106-698-2125
PCT-US02-18947-620
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Sequence 620, App
Sequence 2790, App
Sequence 1790, App
Sequence 1, Appli
Sequence 1962, App
Sequence 173, Appl
Sequence 1141, Ap
Sequence 1412, Appl
Sequence 1412, Appl
Sequence 199, Appl
Sequence 199, Appl
Sequence 424, Appl
Sequence 976, Appl
Sequence 976, Appl
Sequence 678, Appl
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2125, Ap
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US-09-101-518A-1
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US-09-101-518A-1
                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/09101518A
GENERAL INFORMATION:
APPLICANT: Li, Yi
APPLICANT: Li, Yi
TITLE OF INVENTION: Human G-Protein Chemokine Receptor HSATU68
FILE REFERENCE: PF218US
CURRENT APPLICATION NUMBER: US/09/101,518A
CURRENT FILING DATE: 2002-03-18
                                                                                                                                                                                                 Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 1876; Conservative 0
                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: PCT/US96/00499
PRIOR FILING DATE: 1996-01-11
NUMBER OF SEQ ID NOS: 9
                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                                                                                                   LENGTH: 1876
TYPE: DNA
ORGANISM: Homo sapiens
181 GAGGAAGTACGGCCCTGGAAGACTGGCGGGGACAGTTATAGGAGGAGCTGCTCAGAGTAA
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                                                                                          GACGCTCTTCTTCCTGCCCAGGGGTCCCTGGGCCGATGGGATCACGCAGAAGAATGCGAG
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Pred. No. 0;
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CURRENT APPLICATION NUMBER: US/10/106,698
CURRENT FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: PCT/US00/26524
PRIOR FILING DATE: 2000-09-28
PRIOR FILING DATE: 1909-09-29
PRIOR FILING DATE: 1999-09-29
PRIOR APPLICATION NUMBER: US 60/163,280
PRIOR APPLICATION NUMBER: US 60/163,280
PRIOR FILING DATE: 1999-11-03
NUMBER OF SEQ ID NOS: 8564
SOFTWARE: Patentin Ver. 3.0
SEQ ID NO 2125
LENGTH: 1877
TYPE: DNA
ORGANISM: Homo sapiens
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APPLICANT: Ruben et al.
TITLE OF INVENTION: Colon FILE REFERENCE: PA005P1
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                                             Score 1873.2;
Pred. No. 0;
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APPLICANT: ROSetta Inpharmatics:
TITLE OF INVENTION: Diagnosis and Prognosis controls: 175-228
CURRENT APPLICATION NUMBER: PCT/US02/18947
CURRENT FILING DATE: 2002-06-14
PRIOR APPLICATION NUMBER: 60/380,770
PRIOR FILING DATE: 2002-05-14
NUMBER OF SEQ ID NOS: 2699
SEQ ID NO 620
LENGTH: 1670
TYPE: DNA
ORGANISM: Homo sapiens
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: NM_001504
DATABASE ENTRY DATE: 2001-06-18
PCT-US02-18947-620
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PCT-US02-18947-620
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Score 1548.4; Pred. No. 0;

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APPLICANT: MUNGER, William E
APPLICANT: MUNGER, William E
APPLICANT: SUN, Hongwei
APPLICANT: SASAI, Hitoshi
APPLICANT: SASAI, Hitoshi
APPLICANT: YAMAMOTO, Jun
TITLE OF INVENTION: Gene Expression Profiles in
TITLE OF INVENTION: Gene Expression Profiles in
CURRENT APPLICATION NUMBER: PCT/US02/25766
CURRENT FILING DATE: 2002-08-14
DETOES ADDITIONATION NUMBER: PCT/US02/25766
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                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 60/311,837
PRIOR FILING DATE: 2001-08-14
NUMBER OF SEQ ID NOS: 13946
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2790
LENGTH: 1670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2790, Application GENERAL INFORMATION:
                                                Best Local Similarity Matches 1558; Conserv
                                                                                                                                            ORGANISM: HOMO FEATURE:
                                                                                                                               OTHER INFORMATION:
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                                                               Score 1548.4;
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                                  GCTGCCCCAACCAGAGAGGGCTCCAGAGGCAGCCATCGTCTTCCCGCCGGGATTCATCCT
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APPLICANT: He, Yudong
APPLICANT: He, Yudong
APPLICANT: Linsley, Peter
APPLICANT: Mao, Mao
APPLICANT: Roberts, Chris
APPLICANT: Roberts, Chris
APPLICANT: Nao, Mac
APPLICANT: Roberts, Chris
APPLICANT: Van 't Veer, Laura
APPLICANT: Van de Vijver, Marc
APPLICANT: Van de Vijver, Marc
APPLICANT: Bernards, Rene
TITLE OF INVENTION: Diagnosis and Prognosis of
FILE REFERENCE: 9301-175-999
CURRENT APPLICATION NUMBER: US/10/172/118
CURRENT FILING DATE: 2002-06-14
PRIOR APPLICATION NUMBER: 60/380,770
PRIOR FILING DATE: 2002-05-14
NUMBER OF SEQ ID NOS: 2699
SEQ ID NO 620
LENGTH: 1670
TYPE: DNA
ORGANISM: HOMO Saplens
FUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: NM_001504
DATABASE ENTRY DATE: 2001-06-18
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US-10-172-118-620
; Sequence 620, Application
; GENERAL INFORMATION:
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                               GGTCTGAGACCTCAGAGGCCTCCTACTCGGGCTTGTGAGGCCGGAATCCGGGCTCCCCTT
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RESULT 6
US-10-251-686-1
; Sequence 1, Application us,;
; GENERAL INFORMATION:
; APPLICANT: Loetscher, Marcel Moser, Bernhard Oin, Shixin
Charles R
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                                                REFERENCE/DOCKET NUMBER: 7
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
TELEFAX: (617) 861-9340
INFORMATION FOR SEQ ID NO: 1:
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                                                                                                                                          FILING DATE: 20-Sep-2002
CLASSIFICATION: <UNKNOWN>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/829,83
FILING DATE: 31-MAR-1997
APPLICATION NUMBER: US 08/709,83
FILING DATE: 10-SEP-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/251,686
                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                      SEQUENCE
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CITY: Lexington
STATE: MA
COUNTRY: USA
ZIP: 02173
                       LENGTH: 1670 base pa
                                                                                                                  NAME: Brook Esq., David E. REGISTRATION NUMBER: 22,592
STRANDEDNESS:
             TYPE:
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; SEQUENCE DESCRIPTION: SI
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                               TGGACATCCTCATGGACCTGGGCGCTTTGGCCCGCAACTGTGGCCCGAGAAAGCAGGGTAG
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        ACGTGGCCAAGTCGGTCACCTCAGGCCTGGGCTACATGCACTGCTGCCTCAACCCGCTGC
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                       TGGACATCCTCATGGACCTGGGCGCTTTGGCCCGCAACTGTGGCCGAGAAAGCAGGGTAG
Similarity 99.1
50; Conservative
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99.1%;
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Pred. No. 0;
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RESULT 7
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Sequence 962, Application PC/TUS0230182
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PCT-US02-30182-962
                                                                                       APPLICANT: Yamamoto, Jun
TITLE OF INVENTION: Identifying Drugs for and
TITLE OF INVENTION: Gene Expression Profiles
FILE REFERENCE: 44921-5029-01-WO
CURRENT APPLICATION NUMBER: PCT/US02/30182
CURRENT FILING DATE: 2002-09-24
PRIOR APPLICATION NUMBER: 09/960,706
PRIOR FILING DATE: 2001-09-24
NUMBER OF SEO ID NOS: 1124
                                                                                                                                                                                               ; Sequence 962, Application
GENERAL INFORMATION:
APPLICANT: Gene Logic, I
APPLICANT: Munger, Will
APPLICANT: Kulkarni, p
APPLICANT: Getzenberg,
APPLICANT: Waga, Iwao
                              ; SOFTWARE: PatentIn Ver.;
SEQ ID NO 962
; LENGTH: 1293
TYPE: DNA
ORGANISM: Homo sapiens
         FEATURE:
OTHER INFORMATION:
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                            ACCCCCTATCACCTGGTGGTGCTGGTGGACATCCTCATGGACCTGGGCGCCTTTGGCCCGC
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Sequence 19, Application US/10251385

GENERAL INFORMATION:
APPLICANT: Behan, Dominic P.
APPLICANT: Chalmers, Derek T.
APPLICANT: Chalmers, Derek T.
APPLICANT: Liaw, Chen W.
TITLE OF INVENTION: Non-Endogenous, ConstituTITLE OF INVENTION: Nerotein Coupled TITLE OF INVENTION: Receptors
FILE REFERENCE: AREN-0040
CURRENT APPLICATION NUMBER: US/10/251,385
CURRENT APPLICATION NUMBER: US/09/170,496
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US-10-251-385-19
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Best Local Similarity
Matches 1097; Conserv
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; Pred. No. 1.4e-225;
0; Mismatches 0;
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RESULT 9
US-10-251-385-173
Sequence 173, Application US/10251385
GENERAL INFORMATION:
APPLICANT: Behan, Dominic P.
APPLICANT: Chalmers, Derek T.
APPLICANT: Liaw, Chen W.
TITLE OF INVENTION: Non-Endogenous, Constitution of Invention: Protein Coupled TITLE OF INVENTION: Protein Coupled TITLE OF INVENTION: Receptors
FILE REFERENCE: AREN-0040
CURRENT APPLICATION NUMBER: US/10/251,385
CURRENT FILING DATE: 2002-09-20
PRIOR APPLICATION NUMBER: US/09/170,496
PRIOR APPLICATION VERSION 3.1
SOFTWARE: Patentin version 3.1
SOFTWARE: Patentin version 3.1
TYPE: DNA
ORGANISM: Homo sapiens
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Query Match
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CAGGCCTGGGCTACATGCACTGCTGCTCCAACCCGCTGCTCTATGCCTTTGTAGGGGTCA
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APPLICANT: Engelhard, Eric
TITLE OF INVENTION: NOVEL COMPOSITIONS AND MET
FILE REFERENCE: A-71249/RMS/DCF
CURRENT APPLICATION NUMBER: US/10/035,832
CURRENT FILING DATE: 2002-07-22
PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US 09/798,586
PRIOR APPLICATION NUMBER: US 09/798,586
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 1613
SOFTWARE: Patentin version 3.1
SEQ ID NO 1414
LENGTH: 1119
TYPE: DNA
ORGANISM: Homo sapiens
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US-10-035-832-1414
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Best Local Similarity 57.0%;
Matches 507; Conservative
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                                                 CACCTGCCTGGCTGTCTGGGGGGCTCTGCCTTCTTTTCGCCCTCCCAGACTTCATCTTCCT 882
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                                                                                                                                                                                                                                                                                                                                            GGCCGAGGGCTCTGTGGGCTCCTGGGGACCTTCCTCTGCAAAACTGTGATTGCCCT
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                                CCAAGCAGAAACGCATGCCTGGTTCACCTCCCGATTCCTCTACCATGTGGCGGGATTCCT
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Pred. No. 9.4e-42;
0; Mismatches 365;
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US-10-035-832-1413
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LENGTH: 2824
TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                          Best
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CURRENT FILLING DATE: 2002-07-22
PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US 09/798,586
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 1613
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APPLICANT: Engelhard, Eric
TITLE OF INVENTION: NOVEL COMPOSITIONS AND
FILE REFERENCE: A-71249/RMS/DCF
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                                                                                                                                                                                               GGCCGAGGGCTCTGTGGGCTGGGGTCCTGGGGGACCTTCCTCTGCAAAACTGTGATTGCCCCT
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Pred. No. 1.1e-41;
0; Mismatches 365;
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OTHER INFORMATION: "n" a

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US-10-035-832-1412
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                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 09/798,586
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 1613
SOFTWARE: Patentin version 3.1
SEQ ID NO 1412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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                                                                                                                                                        Query Match
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TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS
FILE REFERENCE: A-71249/FMS/DCF
CURRENT APPLICATION NUMBER: US/10/035,832
CURRENT FILING DATE: 2002-07-22
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APPLICANT: Engelhard, E
                                    19830. CTTCAAGGCCGTGTTCGTGCCCGTGGCCTACAGCCTCATCTTCCTCCTGGGCGTGATCGG 19889
                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Homo sapiens
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APPLICANT: Behan, Dominic P.
APPLICANT: Chalmers, Derek T.
APPLICANT: Chalmers, Derek T.
APPLICANT: Liaw, Chen W.
TITLE OF INVENTION: Non-Endogenous, Constitution of Invention: Receptors FILE REFERENCE: AREN-0040
CURRENT APPLICATION NUMBER: US/10/251,385
CURRENT FILING DATE: 2002-09-20
PRIOR APPLICATION NUMBER: US/09/170,496
PRIOR FILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 294
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                RESULT 13
US-10-251-385-65
; Sequence 65, Application US/10251385
; GENERAL INFORMATION:
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LENGTH: 1119
TYPE: DNA
ORGANISM: Homo sapiens
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RESULT 14 US-10-251-385-199

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SEQ ID NO 199
LENGTH: 1119
TYPE: DNA
ORGANISM: Homo sapiens
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GENERAL INFORMATION:
APPLICANT: Behan, Dominic P.
APPLICANT: Chalmers, Derek T.
APPLICANT: Liaw, Chen W.
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PRIOR FILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 294
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TITLE OF INVENTION: Protein-Coupled
TITLE OF INVENTION: Receptors
FILE REFERENCE: AREN-0040
CURRENT APPLICATION NUMBER: US/10/251,385
CURRENT FILING DATE: 2002-09-20
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                                                                                                                                       GCTGCCCCTGCTGGTCATGGCCTACTGCTATGCCCACATCCTGGCCGTGCTG---CTGGT 104
                                                                                                                                                                                                                                                  AGTGGACGCTGCCGTCCAGTGGGTCTTTTGGCTCTGGCCTCTGCAAAGTGGCAGGTGCCCT 702
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APPLICANT: Chenchik, Alex
APPLICANT: Lukashev, Matvey
TITLE OF INVENTION: Hematology/Immunology Array
FILE REFERENCE: CLON-006CIP15
CURRENT APPLICATION NUMBER: US/09/442,384B
CURRENT FILING DATE: 1999-11-17
PRIOR APPLICATION NUMBER: 09/053,375
PRIOR FILING DATE: 1998-03-31
NUMBER OF SEQ ID NOS: 830
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 424
LENGTH: 2818
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 12.7%;
Best Local Similarity 56.9%;
Matches 506; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: homo sapiens
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                   CCTGAACATAGTTCATGCCACCCAGCTCTACCGCCGGGGGGCCCCGGGCCCGGGTGACCCT
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CCAAGCAGAAACGCATGCCTGGTTCACCTCCCGATTCCTCTACCATGTGGCGGGATTCCT
                                                                  CAAAGTCAGCCAAGGCCATCACAACAACTCCCTGCCACGTTGCACCTTCTCCCAAGAGAA
                                                                                                   GTCGGCCCACCACGACGAGCGCCTCAACGC------CACCCACTGCCAATACAA 930
                                                                                                                                     CACCTGTGGGACCATCTGGCTGGTGGGCTTCCTTCCTTGCCTTGCCAGAGATTCTCTTCGC
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GTTCCGCAGTGACCTGTCGCGGCTCCTGACCAAGCTGGGCTGTACCGGCC
                                           GTTCCGGGAGCGGATGTGGATGCTGCTCTTGCGCCTGGGCTGCCCCAACC 1334
                                                                                                           AGGCCTGGGCTACATGCACTGCCTGCCTCAACCCGCTGCTCTATGCCTTTGTAGGGGTCAA 1284
                                                                                                                                                                                                                      CGCTTTGGCCCGCAACTGTGGCCGAGAAAGCAGGGTAGACGTGGCCAAGTCGGTCACCTC 1224
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                                                                                      GTTCCTGGGCCTGGCCTGCTCCAACCCCATGCTCTACACTTTCGCCGGCGTGAA 1067
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Search completed: November 2, 2002, 04:32:28 Job time: 507 secs

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